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OM protein - protein search, using sw model

Run on: April 8, 2004, 14:46:43 ; Search time 41 Seconds  
(without alignments)  
1135.122 Million cell updates/sec

Title: US-09-613-972A-14  
Perfect score: 951  
Sequence: 1 MCLSHLENPLSHSRTOGAQ.....VLKNTYWGIIILLANPQFIS 177

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US09E\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10F\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	12	US-10-202-062-40
2	951	100.0	177	13	US-10-080-455-1
3	951	100.0	177	13	US-10-116-378-16
4	951	100.0	177	14	US-10-151-882-39
5	951	100.0	177	14	US-10-218-547-40
6	951	100.0	177	14	US-10-310-793-44
7	906	95.3	169	9	US-09-345-790-2
8	906	95.3	169	9	US-10-136-511-2
9	608	63.9	113	14	US-10-338-083-17
10	281	29.5	52	9	US-09-864-761-48455
11	85.5	9.0	377	15	US-10-295-027-280
12	79.5	8.0	246	12	US-10-424-599-201262
13	76.5	8.0	1138	14	US-10-261-482-4
14	75.5	7.9	365	12	US-10-425-114-47601
15	75.5	7.9	5795	9	US-09-815-242-12610

Sequence 33, Appl	16	74.5	7.8	271	15	US-10-224-880C-33	Sequence 33, Appl
Sequence 13, Appl	17	74.5	7.8	332	14	US-10-182-960-13	Sequence 13, Appl
Sequence 2, Appl	18	74.5	7.8	543	9	US-09-757-041-2	Sequence 2, Appl
Sequence 35, Appl	19	74.5	7.8	543	15	US-10-004-378A-35	Sequence 35, Appl
Sequence 3816, Ap	20	74.5	7.8	939	15	US-10-369-493-3816	Sequence 3816, Ap
Sequence 225192	21	74	7.8	339	12	US-10-424-599-225192	Sequence 225192
Sequence 1, Appl	22	74	7.8	566	8	US-08-813-323A-1	Sequence 1, Appl
Sequence 7, Appl	23	74	7.8	567	14	US-10-242-212-7	Sequence 7, Appl
Sequence 103, App	24	74	7.8	567	14	US-10-207-655-103	Sequence 103, App
Sequence 2, Appl	25	74	7.8	568	8	US-08-813-323A-2	Sequence 2, Appl
Sequence 166, App	26	74	7.8	568	12	US-10-042-865-166	Sequence 166, App
Sequence 173, App	27	74	7.8	568	15	US-10-116-275-173	Sequence 173, App
Sequence 36, Appl	28	74	7.8	568	15	US-10-004-378A-36	Sequence 36, Appl
Sequence 8130, Ap	29	73.5	7.7	345	12	US-10-335-977-6130	Sequence 8130, Ap
Sequence 6131, Ap	30	73.5	7.7	346	12	US-10-372-686-6	Sequence 6131, Ap
Sequence 6, Appl	31	73.5	7.7	609	14	US-10-371-558-6	Sequence 6, Appl
Sequence 6, Appl	32	73.5	7.7	609	14	US-10-371-558-6	Sequence 6, Appl
Sequence 6129, Ap	33	73	7.7	609	14	US-10-375-553-6	Sequence 6129, Ap
Sequence 231929	34	73	7.7	249	12	US-10-335-977-6129	Sequence 231929
Sequence 17, Appl	35	73	7.7	313	12	US-10-424-599-231929	Sequence 17, Appl
Sequence 73, Appl	36	73	7.7	389	9	US-09-767-041-17	Sequence 73, Appl
Sequence 49, Appl	37	73	7.7	448	15	US-10-354-774-73	Sequence 49, Appl
Sequence 51, Appl	38	73	7.7	448	15	US-10-271-012-73	Sequence 51, Appl
Sequence 53, Appl	39	73	7.7	514	14	US-10-295-074-49	Sequence 53, Appl
Sequence 53, Appl	40	73	7.7	514	14	US-10-295-074-51	Sequence 53, Appl
Sequence 71, Appl	41	73	7.7	514	14	US-10-295-074-59	Sequence 71, Appl
Sequence 71, Appl	42	73	7.7	517	14	US-10-295-074-53	Sequence 71, Appl
Sequence 71, Appl	43	73	7.7	1274	15	US-10-354-774-71	Sequence 71, Appl
Sequence 6, Appl	44	73	7.7	1274	15	US-10-271-012-71	Sequence 6, Appl
	45	73	7.7	1274	15	US-10-452-024-6	

#### ALIGNMENTS

RESULT 1  
US-10-202-062-40  
; Sequence 40, Application US/10202062  
; Publication No. US20040038349A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc..  
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members  
; FILE REFERENCE: PFS59  
; CURRENT APPLICATION NUMBER: US/10/202,062  
; CURRENT FILING DATE: 2002-07-25  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 40  
; TYPE: PRT  
; ORGANISM: human  
US-10-202-062-40

Query Match	100.0%	Score 951	DB 12	Length 177
Best Local Similarity	100.0%	Pred. No. 1.2e-95		
Matches 177	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MCLSHLENPLSHSRTOGAQSSSKMLFCSIVMLLFLCSFSLIFLQLETAKEPCWA	60	
Db	1	MCLSHLENPLSHSRTOGAQSSSKMLFCSIVMLLFLCSFSLIFLQLETAKEPCWA	60	
QY	61	KFGPLPSKQWMASSPPCKVKVSKLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN	120	
Db	61	KFGPLPSKQWMASSPPCKVKVSKLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN	120	
QY	121	KDVIOTLNKSKIQNVGGTYELHVGDTIDLLFNSEHQVLKNTYWGIIILLANPQFIS	177	
Db	121	KDVIOTLNKSKIQNVGGTYELHVGDTIDLLFNSEHQVLKNTYWGIIILLANPQFIS	177	

RESULT 2

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US-10-080-455-1
; Sequence 1, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
; FILE REFERENCE: P1150R2
; CURRENT APPLICATION NUMBER: US/10/080,455
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/195,368
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: US 60/069,661
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/065,635
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-455-1

Query Match      100.0%; Score 951; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
QY 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
DB 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
QY 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177
DB 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177

RESULT 4
US-10-151-882-39
; Sequence 39, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PF554
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 39
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-39

Query Match      100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
QY 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
DB 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
QY 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177
DB 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177

RESULT 5
US-10-218-547-40
; Sequence 40, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases R
; FILE REFERENCE: PFS61
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 40
; LENGTH: 177
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US-10-080-455-1
; Sequence 1, Application US/10080455
; Publication No. US20020146389A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pitti, Robert M.
; TITLE OF INVENTION: DNA19355 Polypeptide, A Tumor Necrosis Factor Homolog
; FILE REFERENCE: P1150R2
; CURRENT APPLICATION NUMBER: US/10/080,455
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 09/195,368
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: US 60/069,661
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: US 60/065,635
; PRIOR FILING DATE: 1997-11-18
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-455-1

Query Match      100.0%; Score 951; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
DB 1 MCLSHLENMPLSHSRTQGAQRSSWKLMFLCSIVMLLFLCSFSLWLIFFIPLQLETAKEPCMA 60
QY 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
DB 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLKLEILQNGLYLYIGVAPNANVNDVAPFEVRLYKN 120
QY 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177
DB 121 KDMIQTTLNKSQKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177

RESULT 3
US-10-116-378-16
; Sequence 16, Application US/10116378
; Publication No. US20020150993A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pitti, Robert M.
; APPLICANT: Wood, William
; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
; TITLE OF INVENTION: NUCLEIC
; FILE REFERENCE: P1206R1
; CURRENT APPLICATION NUMBER: US/10/116,378
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 16
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-378-16
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; TYPE: PRT
; ORGANISM: human
US-10-218-547-40

Query Match      100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCLSHLENMPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCMA 60
Db 1 MCLSHLENMPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCMA 60

Qy 61 KFGPLPSKWQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKN 120
Db 61 KFGPLPSKWQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKN 120

Qy 121 KMIQTLTKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 177
Db 121 KMIQTLTKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 177

RESULT 6
US-10-310-793-44
; Sequence 44, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 44
; LENGTH: 177
; TYPE: PRT
; ORGANISM: human
US-10-310-793-44

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Query Match      100.0%; Score 951; DB 14; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.2e-95;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCLSHLENMPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCMA 60
Db 1 MCLSHLENMPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCMA 60

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Qy 61 KFGPLPSKWQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKN 120
Db 61 KFGPLPSKWQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKN 120

Qy 121 KMIQTLTKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 177
Db 121 KMIQTLTKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 177

RESULT 7
US-09-345-790-2
; Sequence 2, Application US/09345790
; Patent No. US20020099198A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/345,790
; APPLICATION NUMBER: US/09/345,790
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,227
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0470001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 169 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-345-790-2

Query Match      95.3%; Score 906; DB 9; Length 169;
Best Local Similarity 100.0%; Pred. No. 9.6e-91;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCWAKFGLPSK 68
Db 1 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSWLIFFIQLQLETAKEPCWAKFGLPSK 60

Qy 69 WQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKNKMDIQTLT 128
Db 61 WQMASSEPPPCVKNKVDWKLQILQNGLYLIYQVAPNANYNDVAPFEVRLYKNKMDIQTLT 120

Qy 129 NKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 177
Db 121 NKSKIQNVGGTYELHVGDTDLIFNSEHQVLKNTYWGIIILLANPOFIS 169

RESULT 8
US-10-136-511-2
; Sequence 2, Application US/10136511

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; Publication No. US20020168729A1
; GENERAL INFORMATION:
; APPLICANT: Yu Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Human Endokine Alpha and Methods of Use
; FILE REFERENCE: 1488.0470007/ES/PSC
; CURRENT APPLICATION NUMBER: US/10/136,511
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/513,584
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/345,790
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/136,788
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/122,099
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 08/912,227
; PRIOR FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: 60/024,058
; PRIOR FILING DATE: 1996-08-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-136-511-2

Query Match 95.3%; Score 906; DB 13; Length 169;
Best Local Similarity 100.0%; Pred.No. 9.6e-91;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPLSHSTQGAQRSSWKLWLFCSIVMLFLCSFSLWIFLQLETAKEPCMAKFGPLPSK 68
DB 1 MPLSHSTQGAQRSSWKLWLFCSIVMLFLCSFSLWIFLQLETAKEPCMAKFGPLPSK 60
QY 69 WQASSEPPPCVKNKSDWKLEILQNGLYLYGVAPNANYNDVAPFEVRLYKNDMIQTILT 128
DB 61 WQASSEPPPCVKNKSDWKLEILQNGLYLYGVAPNANYNDVAPFEVRLYKNDMIQTILT 120
QY 129 NKSXIQNVGGTYELHVGDTDLIFNSEHQVLYKNTYGIILLANPQFIS 177
DB 121 NKSXIQNVGGTYELHVGDTDLIFNSEHQVLYKNTYGIILLANPQFIS 169

RESULT 9
US-10-338-083-17
; Sequence 17, Application US/10338083
; Publication No. US20030166559A1
; GENERAL INFORMATION:
; APPLICANT: Tansey, Malu Lourdes G.
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof
; FILE REFERENCE: A-71273-2
; CURRENT APPLICATION NUMBER: US/10/338,083
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/345,805
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/373,453
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-338-083-17

Query Match 63.9%; Score 608; DB 14; Length 113;
Best Local Similarity 100.0%; Pred.No. 2.1e-58;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 58 CMAKFGPLPSKQWASSEPPPCVKNKSDWKLEILQNGLYLYGVAPNANYNDVAPFEVRL 117
DB 1 CMAKFGPLPSKQWASSEPPPCVKNKSDWKLEILQNGLYLYGVAPNANYNDVAPFEVRL 60
QY 118 YKNKDMIQTILTNTKSKIQNVGGTYELHVGDTDLIFNSEHQVLYKNTYGIILL 170
DB 61 YKNKDMIQTILTNTKSKIQNVGGTYELHVGDTDLIFNSEHQVLYKNTYGIILL 113

RESULT 10
US-09-864-761-48455
; Sequence 48455, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48455
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031599.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EST HUMAN HIT: BE270854.1, EVALUAE 6.50e-01
; OTHER INFORMATION: SWISSPROT HIT: P25003, EVALUAE 1.20e-00
; US-09-864-761-48455

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Query Match 29.5%; Score 281; DB 9; Length 52;  
Best Local Similarity 100.0%; Pred. No. 4.1e-23;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENPLSRGCGRRSSWKLWFLCSIVMLFLCSFSLIFLQLE 52  
DB 1 MCLSHLENPLSRGCGRRSSWKLWFLCSIVMLFLCSFSLIFLQLE 52

RESULT 11  
US-10-295-027-280  
; Sequence 280, Application US/10295027  
; Publication No. US20030232350A1  
; GENERAL INFORMATION:  
; APPLICANT: Afar, Daniel  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsberg, Wendy M.  
; APPLICANT: Gish, Kurt C.  
; APPLICANT: Glynn, Richard  
; APPLICANT: Hevezi, Peter A.  
; APPLICANT: Mack, David H.  
; APPLICANT: Murray, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
; OF INVENTION: Methods of Screening for Modulators of Cancer  
; FILE REFERENCE: 018501-012500US  
; CURRENT APPLICATION NUMBER: US/10/295,027  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: US 09/663,733  
; PRIOR FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: US 60/350,666  
; PRIOR FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/335,394  
; PRIOR FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/332,464  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: US 60/334,393  
; PRIOR FILING DATE: 2001-11-29  
; PRIOR APPLICATION NUMBER: US 60/340,376  
; PRIOR FILING DATE: 2001-12-14  
; PRIOR APPLICATION NUMBER: US 60/347,211  
; PRIOR FILING DATE: 2002-01-08  
; PRIOR APPLICATION NUMBER: US 60/347,349  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 60/355,250  
; PRIOR FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: US 60/356,714  
; PRIOR FILING DATE: 2002-02-13  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 280  
; LENGTH: 377  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-295-027-280

Query Match 9.0%; Score 85.5; DB 15; Length 377;  
Best Local Similarity 20.8%; Pred. No. 1.3;  
Matches 32; Conservative 31; Mismatches 54; Indels 37; Gaps 6;

QY 26 LWLFCSIVM--LLFLCSFSLIFLQLETAKEPCMAKFGPLPSKWQMASSEPPCUNKVS 83  
DB 127 IFWCKLVNPSAININFLNLLLELLMAATVIA-----ARSEEDCKKK-- 174

QY 84 DWKLEILQNGLYGVAPNANDVAPFVRVLYKNDMIQTITNSKIQNVGGTYVELH 143  
DB 175 -----KGSMSDSANILDEVPPFARVLKSYSVVEVIAGISAV--LGGIILN 218

QY 144 VGDITDILFNSEHQVLYKNTVWGIILANPOFIS 177  
DB 219 VDDSV-----SGPHLSV---TFFWILVACFPISA 245

RESULT 12  
US-10-424-599-201262  
; Sequence 201262, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 201262  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(246)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23765C.1.pep  
US-10-424-599-201262

Query Match 8.4%; Score 79.5; DB 12; Length 246;  
Best Local Similarity 22.9%; Pred. No. 3.3;  
Matches 36; Conservative 21; Mismatches 55; Indels 45; Gaps 6;

QY 22 SSKWLFCFSIVMLFLCSFSLIFLQLETAKEPCMAKFGPLPSKWQMASSEPP----- 77  
DB 88 SKWKLEL-----AWLT---KALEPALQFCB---WALPTGNGIGNKPPPSNRS 128

QY 78 -----CVNK-----VSDWKLEILQNGLYLYGVAPNANDVAPFVRVLYKNDMIOTL 127  
DB 129 LTEIIACIORSKIGIQDWSLSDLATIGLYLYLQRASTHPFEDIKGIQI----- 176

QY 128 TNKSKIQNVGGTYVELHVGDTIDILFNSEHQVLYKNTY 164  
DB 177 LSESIVQDLIVHIELAKGAYRDNPFSLSRNCMLRESY 213

RESULT 13  
US-10-261-482-4  
; Sequence 4, Application US/10261482  
; Publication No. US20030036089A1  
; GENERAL INFORMATION:  
; APPLICANT: WEI, Ming-Hui et al  
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED  
; OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL000869CON  
; CURRENT APPLICATION NUMBER: US/10/261,482  
; CURRENT FILING DATE: 2002-10-02  
; PRIOR APPLICATION NUMBER: 09/684,393  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: 60/172,600  
; PRIOR FILING DATE: 1999-12-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1138  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-10-261-482-4

Query Match 8.0%; Score 76.5; DB 14; Length 1138;  
Best Local Similarity 22.2%; Pred. No. 5.1;  
Matches 40; Conservative 21; Mismatches 46; Indels 73; Gaps 7;

QY 33 VMLFLCFSWL-----IFILQLETAKEPCWAKFGPLFSKWQMASSEF 76  
Db 345 VYQLQSGFQWVWAAIGSDDEYGRQGLSIFGALAAAGICIAHEGLVP-----LPRADD 400  
QY 77 PCVKNYSQWKLILONGLY-----LI-----YGOVAPNA----- 105  
Db 401 SRLGKVODVLHVQVNGSGLGARGICAVPRDRQQSVWISLIGSYDYGQGVQALAEUA 460  
QY 106 -----NYNDVAPFEVRL--YKNKDMIQTLTKSKIQNVGGTYELHVGDTIDILFNSHP 156  
Db 461 VPRGICVAFKDIIVFSAVGRDPRMQSMQHLAQCSSVQVV-----LLFASVH 507

RESULT 14  
US-10-425-114-47601  
; Sequence 47601, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 47601  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700152776\_FLI.pep  
US-10-425-114-47601

Query Match 7.9%; Score 75.5; DB 12; Length 365;  
Best Local Similarity 18.4%; Pred. No. 15;  
Matches 39; Conservative 33; Mismatches 51; Indels 89; Gaps 9;

QY 10 PLSHRTGGAQRSSKWLWFC-----SIVMLFLCFSWLIFILQLETAKEPCWAKFGPL 65  
Db 61 PCSYRRSDPFKLG:WNNYLSVEKRSIVRLF----- 92  
QY 66 PSKWQMASSEPP-----CVNKYSD-----WKLEILONGLYLY 98  
Db 93 PEPGRVAKQPLARFLRLVSWAGPPRSVCSPVHEHLRLTSDDFVQVQDAMSGRFTI- 151  
QY 99 QGVAPNANYNDVAPFEVRL-----YKNKDMIQTLTKSKIQNVGGTYELHVGDT 147  
Db 152 -----DVEFLDLRIATNATESSSVWPNFEGMVQKIASKAL-----GCLSRMLADS 197  
QY 148 I--DLIFNSEHQVKNQNTYWGILLANPQFIS 177  
Db 198 IHADVTTINTDGVLR--AKKAVLAACSPVFKS 227

RESULT 15  
US-09-815-242-12610  
; Sequence 12610, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12610  
; LENGTH: 5795  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-09-815-242-12610

Query Match 7.9%; Score 75.5; DB 9; Length 5795;  
Best Local Similarity 27.4%; Pred. No. 5.5e+02;  
Matches 31; Conservative 17; Mismatches 40; Indels 25; Gaps 6;

QY 65 LPSKWQMASSEPPCVNKVSDWKLEILONGLYLYIGQVAPNANYNDVAPFEVRLYKNKDMI 124  
Db 952 LPSGWTSLTK-----SDNK-----NGSLAITGRYSMNQAFNSDITFKV---SATDNV 996  
QY 125 QTLTKSKIQNVGGTYELHVGDTIDILFNSHQVKNQNTYWGILLANPQFIS 177  
Db 997 NNTTNDSSQKHV-----SIHVSK-----ISEDAPIVLGN--EKVVVNPPTAVS 1039

Search completed: April 8, 2004, 14:52:47  
Job time : 41 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 8, 2004, 14:44:52 ; Search time 59 Seconds  
(without alignments)  
847.643 Million cell updates/sec

Title: US-09-613-972A-14

Perfect score: 951  
Sequence: 1 MCLSHLENPLSHSRITQGAQ.....VLKNTYWGIIILANPQFIS 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	2	AA15817 Amino aci
2	951	100.0	177	2	AA15817 Amino aci
3	951	100.0	177	2	AA15817 Amino aci
4	951	100.0	177	4	AA15817 Amino aci
5	951	100.0	177	4	AA15817 Amino aci
6	951	100.0	177	4	AA15817 Amino aci
7	951	100.0	177	4	AA15817 Amino aci
8	951	100.0	177	5	AA15817 Amino aci
9	951	100.0	177	6	AA15817 Amino aci
10	951	100.0	177	6	AA15817 Amino aci
11	951	100.0	177	7	AA15817 Amino aci
12	906	95.3	169	2	AA15817 Amino aci
13	906	95.3	169	3	AA15817 Amino aci
14	906	95.3	169	3	AA15817 Amino aci
15	906	95.3	169	6	AA15817 Amino aci
16	906	95.3	169	7	AA15817 Amino aci
17	566	59.5	508	4	AA15817 Amino aci
18	281	29.5	52	4	AA15817 Amino aci
19	85.5	9.0	377	4	AA15817 Amino aci
20	85.5	9.0	377	5	AA15817 Amino aci
21	85.5	9.0	377	5	AA15817 Amino aci
22	85.5	9.0	441	4	AA15817 Amino aci
23	84.5	8.6	1221	7	AA15817 Amino aci
24	82	8.6	1188	3	AA15817 Amino aci
25	81	8.5	162	4	AA15817 Amino aci

26	81	8.5	162	6	ABM54419 Propionib
27	80.5	8.5	107	6	ABM64618 Propionib
28	79.5	8.4	851	5	ABM93512 Herbicida
29	79.5	8.4	879	5	ABM93594 Fungal ZB
30	79	8.3	1013	7	ABM90688 Novel pro
31	78.5	8.3	599	5	ABM25933 Streptoco
32	78	8.2	105	4	ABM62280 Human gen
33	77.5	8.1	226	5	ABM83970 Human U2
34	77.5	8.1	880	5	ABM35593 Fungal ZB
35	77.5	8.1	3614	4	ABM62664 Drosophil
36	77	8.1	183	3	ABM43533 Arabidops
37	77	8.1	228	3	ABM43532 Arabidops
38	77	8.1	230	3	ABM43531 Arabidops
39	77	8.1	326	1	ABM60547 Segment 8
40	77	8.1	326	7	ABM36761 Rhesus ro
41	77	8.1	2763	2	ABM10344 Maize dwa
42	76.5	8.0	1138	5	ABM21502 1138-mer
43	76.5	8.0	1138	6	ABM62107 Rat taste
44	76	8.0	208	5	ABM54205 Lactococc
45	75.5	7.9	550	2	ABM71468 Cercospor

## ALIGNMENTS

RESULT 1  
AA15817  
ID AA15817 standard; protein; 177 AA.  
XX  
AC AA15817;  
XX  
DT 28-JUL-1999 (first entry)  
XX  
DE Amino acid sequence of human DNA19355 polypeptide.  
XX  
KW DNA19355; tumour necrosis factor homologue; receptor GTR; immunogen;  
KW antibody; apoptosis; mammalian cancer cell;  
KW tumour necrosis factor (TNF)-alpha secretion; primary T- cell;  
KW proinflammatory response.  
XX  
OS Homo sapiens.  
XX  
PN WO925834-A1.  
XX  
PD 27-MAY-1999.  
XX  
PF 18-NOV-1998; 98WO-US024621.  
XX  
PR 18-NOV-1997; 97US-0065635P.  
PR 12-DEC-1997; 97US-0069661P.  
XX  
(GETH ) GENENTECH INC.  
PI Ashkenazi AJ, Gurney AL, Marsters SA, Pitti R, Baker KP;  
PI Godowski PJ, Mark MR;  
PI WPI; 1999-338009/28.  
XX  
PT N-PSDB; AAX59744.  
XX  
PS New DNA19355 polypeptide as tumour necrosis factor homolog.  
XX  
PS Claim 10; Fig 1; 86pp; English.

*proposed name*

The present sequence represents a polypeptide designated DNA19355. The polypeptide is a tumour necrosis factor homologue. The DNA19355 polynucleotide sequence can be used to derive hybridisation probes for e.g. isolating similar sequences, gene mapping, genetic analysis, etc. Nucleic acids which encode DNA19355 can also be used to generate transgenic or knockout animals, which are useful in the development and screening of therapeutically useful reagents. The DNA19355 polypeptides may be used in diagnostic assays to detect the presence of the receptor GTR in mammalian tissues. The polypeptides can also be used as immunogens to raise antibodies. The polypeptides may also be used to

CC induce apoptosis in mammalian cancer cells. DNA19355 polypeptides  
CC stimulate secretion of tumour necrosis factor (TNF)-alpha in primary T-  
CC cells, and so can be used to stimulate a proinflammatory response in  
CC mammalian cells  
XX  
SQ Sequence 177 AA;  
  
Query Match 100.0%; Score 951; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCLSHLENMPLSHSRTOGAORSSWKWLFCSIVMLLFLCSFSLIFIFLOLETAKEPCMA 60  
Db 1 MCLSHLENMPLSHSRTOGAORSSWKWLFCSIVMLLFLCSFSLIFIFLOLETAKEPCMA 60  
  
QY 61 KFGPLPSKQWQWASSEPPCVNKNVSDWKLEILLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN 120  
Db 61 KFGPLPSKQWQWASSEPPCVNKNVSDWKLEILLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN 120  
  
QY 121 KDMIQTLTNKSKIQNVGTYVELHVGDTIDIFNSEHQLVKNNTYWGIIILLANPOFIS 177  
Db 121 KDMIQTLTNKSKIQNVGTYVELHVGDTIDIFNSEHQLVKNNTYWGIIILLANPOFIS 177  
  
RESULT 2  
AAY06646  
ID AAY06646 standard; protein; 177 AA.  
AC AAY06646;  
XX  
XX 26-OCT-1999 (first entry)  
XX Human PRO364 ligand.  
XX  
KW PRO364 ligand; tumour necrosis factor receptor; human; apoptosis;  
KW inflammation; antiinflammatory; NF-KB activation; autoimmune disease;  
KW therapy.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
PH Domain 1..25 "cytoplasmic domain"  
FT Domain 26..51  
FT Domain /note= "transmembrane domain"  
FT Domain 52..177  
FT Modified-site 129 /note= "extracellular domain"  
FT Modified-site 161 /note= "N-glycosylation"  
FT Modified-site /note= "N-glycosylation"  
XX  
XX WO9940196-A1.  
XX  
XX 12-AUG-1999.  
XX  
XX 09-FEB-1999; 99WO-US002642.  
XX  
XX 09-FEB-1998; 98US-0074087P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Gurney AL, Marsters SA, Pitti RM, Wood WT;  
XX Goddard A;  
XX WPI; 1999-494296/41.  
XX DR N-PSDB; AAX87726.  
XX  
XX Tumour necrosis factor receptor homologue - useful for, e.g. modulating  
XX apoptosis and NF-KB activation and proinflammatory or autoimmune  
XX responses.  
XX  
XX Example 2; Fig 5A; 104pp; English.  
PS

XX The present sequence represents a putative ligand for PRO364 (see also  
CC AAY06605), a novel member of the tumour necrosis factor receptor family.  
CC The sequence was deduced from an isolated cDNA clone (see AAX87726).  
CC Hypoathy analysis suggests a type II transmembrane homology. The  
CC mol.wt. is 20,308. Identity is shown to human Apo-2L (19.8%), Fas/Apol-  
CC ligand (19.0%), TNF-alpha (20.6%) and lymphotoxin-alpha (17.5%). PRO364  
CC is useful for modulating apoptosis, NF-KB activation and proinflammatory  
CC or autoimmune responses in mammalian cells  
XX  
SQ Sequence 177 AA;  
  
Query Match 100.0%; Score 951; DB 2; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCLSHLENMPLSHSRTOGAORSSWKWLFCSIVMLLFLCSFSLIFIFLOLETAKEPCMA 60  
Db 1 MCLSHLENMPLSHSRTOGAORSSWKWLFCSIVMLLFLCSFSLIFIFLOLETAKEPCMA 60  
  
QY 61 KFGPLPSKQWQWASSEPPCVNKNVSDWKLEILLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN 120  
Db 61 KFGPLPSKQWQWASSEPPCVNKNVSDWKLEILLQNGLYLIYGQVAPNANYNDVAPFEVRLYKN 120  
  
QY 121 KDMIQTLTNKSKIQNVGTYVELHVGDTIDIFNSEHQLVKNNTYWGIIILLANPOFIS 177  
Db 121 KDMIQTLTNKSKIQNVGTYVELHVGDTIDIFNSEHQLVKNNTYWGIIILLANPOFIS 177  
  
RESULT 3  
AAB47056  
ID AAB47056 standard; protein; 177 AA.  
XX  
XX AAB47056;  
AC AAB47056;  
XX  
XX 08-MAY-2001 (first entry)  
DT  
DE PRO175.  
XX  
XX PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor;  
KW hGTR; ligand; hGTRL; PRO175; tumour necrosis factor receptor; TNFR;  
KW human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy;  
KW myocardial infarction; FGF 2alpha; trauma; cancer; angiogenesis;  
KW age-related macular degeneration; antibody; cancer; periodontal disease;  
KW vascular-related drug targeting; atherosclerosis; hypertension;  
KW inflammatory vasculitides; Reynaud's disease; aneurysm;  
KW arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;  
KW fibrosis; neuropathy; rheumatoid arthritis.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
PH Region 1..25  
FT Region /note= "Cytoplasmic region"  
FT Region 26..51  
FT Region /note= "Transmembrane region"  
FT Region 52..177  
FT Modified-site 129 /note= "Extracellular region"  
FT Modified-site 161 /note= "N-glycosylated"  
FT Modified-site /note= "N-glycosylated"  
XX  
XX WO200103720-A2.  
XX  
XX 18-JAN-2001.  
XX  
XX 11-JUL-2000; 2000WO-US018867.  
XX  
XX 12-JUL-1999; 99US-0143304P.  
XX  
XX (GETH ) GENENTECH INC.  
XX



PI Williams PM, Gerritsen ME;  
 XX WPI; 2001-138257/14.  
 DR N-PSDB; AAC65435.  
 XX  
 PT Composition for diagnosing and treating cardiovascular, endothelial and  
 PT angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.  
 PS Claim 2; Fig 5; 76pp; English.  
 XX  
 CC This sequence represents PRO175 polypeptide, which is a human gluco-  
 CC corticoid-induced tumor necrosis factor ligand (hGIFRL). The  
 CC corresponding receptor (hGIFR), PRO364, is given in AAB47054. PRO364 and  
 CC PRO175 may be used in a mixture with a cardiovascular, endothelial,  
 CC angiogenic or angiostatic agent for the treatment of a cardiovascular,  
 CC endothelial, angiogenic or angiostatic disorder. The PRO364 sequence was  
 CC isolated from an expressed sequence tag (EST) database as having homology  
 CC to members of the tumor necrosis factor receptor (TNFR) family of  
 CC polypeptides. The PRO175 cDNA sequence was isolated from a library of  
 CC cDNA fragments derived from human umbilical vein endothelial cells  
 CC (HUVEC). Administering an effective amount of PRO364 or PRO175 or their  
 CC antagonists is useful for treating cardiac hypertrophy (which is  
 CC initiated by myocardial infarction and characterized by the presence of  
 CC an elevated level of PGP 2alpha), trauma, a cancer, or age-related  
 CC macular degeneration in a human. Administering a therapeutically  
 CC effective amount of an antibody that binds PRO364 or PRO175 is useful for  
 CC inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering  
 CC from a tumor or a retinal disorder. PRO364 or PRO175, or their  
 CC antagonists, are useful for vascular-related drug targeting or as  
 CC therapeutic targets for the treatment or prevention of atherosclerosis,  
 CC hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms,  
 CC arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection  
 CC or regeneration and treatment of lung or liver fibrosis, periodontal  
 CC diseases, attraction of bone-forming cells, central and peripheral  
 CC nervous system disease and neuropathies and rheumatoid arthritis  
 XX  
 SQ Sequence 177 AA;  
 Query Match 100.0%; Score 951; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCLSHLENPLSHRTQGRSQRSWKWLFCSIVMLFLCSFWLFIPLQLETAKEPCMA 60  
 Db 1 MCLSHLENPLSHRTQGRSQRSWKWLFCSIVMLFLCSFWLFIPLQLETAKEPCMA 60  
 QY 61 KFGPLPSKQMASSEPPCVNKYSDWKLEILQGLYLYIGVAPNANYNDVAFVEVLYKN 120  
 Db 61 KFGPLPSKQMASSEPPCVNKYSDWKLEILQGLYLYIGVAPNANYNDVAFVEVLYKN 120  
 QY 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGIIILANPQFIS 177  
 Db 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGIIILANPQFIS 177  
 RESULT 4  
 AAB20109  
 ID AAB20109 standard; protein; 177 AA.  
 XX  
 AC AAB20109;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO175.  
 XX  
 KW PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;  
 KW antiarthritic; antiinflammatory; antianaemic; immunosuppressive;  
 KW antihypertoid; antidiabetic; neuroprotective; hepatotropic; virucide;  
 KW dermatological; antipsoriatic; antiasthmatic; anti allergic;  
 XX immunostimulant.  
 OS Homo sapiens.  
 XX  
 XX

PH Key Location/Qualifiers  
 FT Peptide 1..44  
 FT /label= Signal\_peptide  
 FT Modified-site 18..24  
 FT /note= "N-myristoylation site"  
 FT Protein 45..177  
 FT /label= Mature\_protein  
 FT Modified-site 129..133  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 161..165  
 FT /note= "Asn is N-glycosylated"  
 XX WO200105972-A1.  
 PN 25-JAN-2001.  
 XX  
 PD 15-MAR-2000; 2000WO-US006884.  
 PF 20-JUL-1999; 99US-0144758P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;  
 PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;  
 PI Watanabe CK, Wood WI;  
 XX WPI: 2001-103149/11.  
 DR N-PSDB; RAF30051.  
 XX  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes.  
 PS Claim 20; Fig 4; 127pp; English.  
 XX  
 CC The present sequence is that of PRO175 (UNQ149), a novel human  
 CC immunomodulator protein (20 kDa, pI 8.08) showing homology to tumour  
 CC necrosis factor family members. The invention provides polynucleotides  
 CC (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20)  
 CC including PRO175. Claimed compositions comprising these proteins or their  
 CC agonists are useful for increasing infiltration of inflammatory cells  
 CC into a tissue of a mammal, stimulating or enhancing an immune response in  
 CC a mammal, or increasing the proliferation of T-lymphocytes in a mammal in  
 CC response to an antigen. Claimed compositions comprising the PRO  
 CC polypeptide or its antagonist have the opposite effect. A claimed method  
 CC for treating an immune related disorder, such as a T cell disorder,  
 CC involves administering the PRO polypeptide, an agonist antibody or an  
 CC antagonist antibody. The disorder is selected from systemic lupus  
 CC erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic  
 CC arthritis, spondyloarthritis, systemic sclerosis, idiopathic  
 CC inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,  
 CC sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,  
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinated diseases (such as multiple sclerosis), autoimmune chronic  
 CC active hepatitis, primary biliary cirrhosis, granulomatous hepatitis,  
 CC sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis  
 CC and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease,  
 CC (auto)immune-mediated skin diseases (such as bullous skin disease,  
 CC erythema multiforme and psoriasis), allergic diseases (such as asthma,  
 CC allergic rhinitis, atopic dermatitis, food hypersensitivity and  
 CC urticaria), immunologic diseases of the lung and transplantation  
 CC associated diseases (such as graft rejection and graft-versus-host  
 CC disease) (all claimed). Claimed methods of diagnosing these disorders  
 CC comprise detecting the level of expression of the PRO gene. Also claimed  
 CC are a method of identifying a compound capable of inhibiting the  
 CC expression or activity of the PRO polypeptide, vectors, host cells,  
 CC antibodies, and a method of stimulating an immune response in a mammal  
 CC using PRO179  
 SQ Sequence 177 AA;  
 Query Match 100.0%; Score 951; DB 4; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCLSHLENPLSHRTQGRSQRSWKWLFCSIVMLFLCSFWLFIPLQLETAKEPCMA 60  
 Db 1 MCLSHLENPLSHRTQGRSQRSWKWLFCSIVMLFLCSFWLFIPLQLETAKEPCMA 60  
 QY 61 KFGPLPSKQMASSEPPCVNKYSDWKLEILQGLYLYIGVAPNANYNDVAFVEVLYKN 120  
 Db 61 KFGPLPSKQMASSEPPCVNKYSDWKLEILQGLYLYIGVAPNANYNDVAFVEVLYKN 120  
 QY 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGIIILANPQFIS 177  
 Db 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGIIILANPQFIS 177  
 RESULT 4  
 AAB20109  
 ID AAB20109 standard; protein; 177 AA.  
 XX  
 AC AAB20109;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO175.  
 XX  
 KW PRO175; UNQ149; human; immune disease; autoimmune disease; antirheumatic;  
 KW antiarthritic; antiinflammatory; antianaemic; immunosuppressive;  
 KW antihypertoid; antidiabetic; neuroprotective; hepatotropic; virucide;  
 KW dermatological; antipsoriatic; antiasthmatic; anti allergic;  
 XX immunostimulant.  
 OS Homo sapiens.  
 XX  
 XX

Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MCLSHLENNPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSLWLIFFIQLQLETAKEPCMA 60
Db	1 MCLSHLENNPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSLWLIFFIQLQLETAKEPCMA 60
QY	61 KFGPLPSKWQWASSPPCVNKVSDWKLLEILQNGLLIYGQVAPNANYNDVAPFEVRLYKN 120
Db	61 KFGPLPSKWQWASSPPCVNKVSDWKLLEILQNGLLIYGQVAPNANYNDVAPFEVRLYKN 120
QY	121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHQVLKNTYWGIIILANPQFIS 177
Db	121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHQVLKNTYWGIIILANPQFIS 177
RESULT 5	
AAB47287	
ID	AAB47287 standard; protein; 177 AA.
AC	AAB47287;
DT	28-FEB-2001 (first entry)
DE	Human angiogenesis-associated protein PRO175, SEQ ID NO:9.
XX	Human; angiogenesis-associated protein; PRO; endothelial cell growth;
KW	cardiac hypertrophy; cardiovascular disorder; endothelial disorder;
KW	angiogenic disorder; atherosclerosis; osteoporosis; hypertension;
KW	myocardial infarction; diabetic retinopathy; rheumatoid arthritis;
KW	Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;
KW	Alzheimer's disease; Huntington's disease; stroke; drug screening;
XX	gene therapy; transgenic animal.
OS	Homo sapiens.
XX	WO200053753-A2.
XX	14-SEP-2000.
XX	05-JAN-2000; 2000WO-US000219.
XX	08-MAR-1999; 99WO-US005028.
PR	12-MAR-1999; 99US-0123957P.
PR	14-MAY-1999; 99US-0134287P.
PR	02-JUN-1999; 99WO-US012252.
PR	23-JUN-1999; 99US-0141037P.
PR	20-JUL-1999; 99US-0144758P.
PR	26-JUL-1999; 99US-0145698P.
PR	01-SEP-1999; 99WO-US020111.
PR	08-SEP-1999; 99WO-US020594.
PR	15-SEP-1999; 99WO-US021090.
PR	15-SEP-1999; 99WO-US021547.
PR	05-OCT-1999; 99WO-US021089.
PR	30-NOV-1999; 99WO-US028313.
PR	30-NOV-1999; 99WO-US028409.
PR	02-DEC-1999; 99WO-US028564.
PR	02-DEC-1999; 99WO-US028565.
XX	(GETH ) GENENTECH INC.
PA	
XX	Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
PI	Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
PI	Pacini NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
XX	WPI; 2001-090793/10.
DR	N-PSDB; AAC97374.
XX	
XX	New isolated nucleic acid for producing a PRO polypeptide, analyzing
PT	genetic disorders and treating cardiovascular, endothelial or angiogenic
PT	disorders, such as atherosclerosis, wounds or cancer.
XX	Claim 69; Fig 4; 293pp; English.
PS	
XX	

Query Match 100.0%; Score 951; DB 4; Length 177;	
Best Local Similarity 100.0%; Pred. NO. 3.9e-97;	
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MCLSHLENNPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSLWLIFFIQLQLETAKEPCMA 60
Db	1 MCLSHLENNPLSHRTQGAQRSSWKLWLFCSIVMLLFLCSFSLWLIFFIQLQLETAKEPCMA 60
QY	61 KFGPLPSKWQWASSPPCVNKVSDWKLLEILQNGLLIYGQVAPNANYNDVAPFEVRLYKN 120
Db	61 KFGPLPSKWQWASSPPCVNKVSDWKLLEILQNGLLIYGQVAPNANYNDVAPFEVRLYKN 120
QY	121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHQVLKNTYWGIIILANPQFIS 177
Db	121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLI FNSHQVLKNTYWGIIILANPQFIS 177
RESULT 6	
AAB47287	
ID	AAB47287 standard; protein; 177 AA.
AC	AAB47287;
XX	
DT	22-AUG-2001 (first entry)
XX	
DE	PRO175 polypeptide.
XX	PRO; type II transmembrane protein; tumour necrosis factor; stroke;
KW	heart hypertrophy; cardiovascular; endothelial; angiogenic; disorder;
KW	myocardial infarction; cardiac hypertrophy; Pgf_alpha; trauma; bone;
KW	cancer; age-related macular degeneration; wound; burn; hypertension;
KW	diabetes mellitus; osteoporosis; ischaemia; atherosclerosis; psoriasis;
KW	rheumatoid arthritis; Crohn's disease; amyloidotic lateral sclerosis;
KW	endometriosis; angina; neoplasms; periodontal disease; cartilage; TNF;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease.
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FT	Peptide 1..25

FT Modified-site /label= Signal peptide  
 FT 18..24  
 FT /label= N-myristoylation site  
 FT Protein 26..177  
 FT /label= Mature PRO175  
 FT Domain 26..51  
 FT /label= Transmembrane domain  
 FT Domain 52..177  
 FT /label= Extracellular domain  
 FT Modified-site 129..133  
 FT /label= N-linked glycosylation site  
 FT Modified-site 161..165  
 FT /label= N-linked glycosylation site  
 XX  
 XX WC200140464-A1.  
 XX  
 XX 07-JUN-2001.  
 XX  
 XX 11-AUG-2000; 2000WO-US022031.  
 XX 30-NOV-1999; 99WO-US028313.  
 XX 30-NOV-1999; 99WO-US028409.  
 XX 05-JAN-2000; 2000WO-US000219.  
 XX 24-FEB-2000; 2000WO-US005004.  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX 17-MAY-2000; 2000WO-US013705.  
 XX 30-MAY-2000; 2000WO-US014941.  
 XX 28-JUL-2000; 2000WO-US020710.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Godowski PJ, Gurney AL;  
 XX Hillan KJ, Mark MR, Marsters SA, Paoni NF, Pitti RM, Wood WT;  
 XX  
 XX WPI; 2001-381383/40.  
 XX N-PSDB; AAC85945.  
 XX  
 XX Isolated PRO polypeptide useful in treating and diagnosing a  
 XX cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes  
 XX mellitus, myocardial infarction, arthritis.  
 XX  
 XX Claim 56; Fig 2; 144pp; English.  
 XX  
 XX The sequences given in AAB47287-90 show PRO polypeptides. PRO175 shows  
 XX type II transmembrane protein typology, and portions of PRO364 show  
 XX homology to members of the tumour necrosis factor (TNF) family, thereby  
 XX indicating that it may be a novel member of the TNF family. PRO175 and  
 XX PRO185 stimulated heart hypertrophy. PRO cDNA's may be used to identify a  
 XX compound that inhibits PRO, diagnosing a cardio-vascular, endothelial or  
 XX angiogenic disorder in a mammal by detecting PRO cDNA, treating  
 XX cardiovascular, endothelial or angiogenic disorder in a mammal, and  
 XX inducing cardiac hypertrophy or inhibiting endothelial cell growth or  
 XX angiogenesis in a mammal. The mammal is a human which has suffered  
 XX myocardial infarction, cardiac hypertrophy characterized by the presence  
 XX of elevated BGF-2alpha, trauma, cancer or age-related macular  
 XX degeneration. Trauma includes wounds or burns. Other treatable diseases  
 XX include diabetes mellitus, osteoporosis, ischaemia, hyper-tension,  
 XX rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis,  
 XX endometriosis, angina, neoplasms, periodontal disease, bone and cartilage  
 XX repair, Alzheimer's disease, Parkinson's disease, Huntington's disease,  
 XX amyotrophic lateral sclerosis, and stroke  
 XX  
 XX Sequence 177 AA;  
 XX  
 XX Query Match 100.0%; Score 951; DB 4; Length 177;  
 XX Best Local Similarity 100.0%; Pred. NO. 3.9e-37;  
 XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 MCLSHLENNPLSHRTGQAGSSWKLMLFCSIVMLLFLCSFSLIFLQLETAKEPCMA 60  
 XX  
 XX 1 MCLSHLENNPLSHRTGQAGSSWKLMLFCSIVMLLFLCSFSLIFLQLETAKEPCMA 60

Qy 61 KFGPLPSKQWQASSEPPCVNKNVSDWKLLELLQNGLYLIYGQVAPNANVNDVAPPEVRLYN 120  
 Db 61 KFGPLPSKQWQASSEPPCVNKNVSDWKLLELLQNGLYLIYGQVAPNANVNDVAPPEVRLYN 120  
 Qy 121 KDMIQTLTNKSQIONVGGTYELHVGDTIDLFNSEHQVLKQNTYWGHIILANQFIS 177  
 Db 121 KDMIQTLTNKSQIONVGGTYELHVGDTIDLFNSEHQVLKQNTYWGHIILANQFIS 177  
 RESULT 7  
 AAB50979  
 ID AAB50979 standard; protein; 177 AA.  
 XX  
 XX AAB50979;  
 XX  
 XX 21-MAR-2001 (first entry)  
 XX  
 XX Human PRO175 protein.  
 XX  
 XX Human; PRO; cardiant; antiangiogenic; antiarteriosclerotic; hypotensive;  
 XX vasotropic; antirheumatic; antiarthritic; antiinflammatory; cytostatic;  
 XX vulnery; antianginal; gene therapy; cardiovascular disease;  
 XX endothelial disorder; angiogenic disorder; cancer; periodontal disease;  
 XX wound healing.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200073445-A2.  
 XX  
 XX 07-DEC-2000.  
 XX  
 XX 17-MAY-2000; 2000WO-US013705.  
 XX  
 XX 02-JUN-1999; 99WO-US012252.  
 XX 23-JUN-1999; 99US-0141037P.  
 XX 20-JUL-1999; 99US-0144758P.  
 XX 26-JUL-1999; 99US-0145698P.  
 XX 28-JUL-1999; 99US-0146222P.  
 XX 01-SEP-1999; 99WO-US020111.  
 XX 30-NOV-1999; 99WO-US028313.  
 XX 30-NOV-1999; 99WO-US028409.  
 XX 02-DEC-1999; 99WO-US028565.  
 XX 16-DEC-1999; 99WO-US0310095.  
 XX 05-JAN-2000; 2000WO-US000219.  
 XX 06-JAN-2000; 2000WO-US000376.  
 XX 11-FEB-2000; 2000WO-US003565.  
 XX 18-FEB-2000; 2000WO-US004341.  
 XX 18-FEB-2000; 2000WO-US004342.  
 XX 24-FEB-2000; 2000WO-US005004.  
 XX 02-MAR-2000; 2000WO-US005841.  
 XX 10-MAR-2000; 2000WO-US006319.  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX 21-MAR-2000; 2000WO-US007532.  
 XX 30-MAR-2000; 2000WO-US008439.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen ME;  
 XX Goddard A, Godowski PJ, Gurney AL, Kuc SS, Mark MR, Marsters SA;  
 XX Paoni NF, Pitti RM, Watanabe CK, Williams PW, Wood WT;  
 XX  
 XX WPI; 2001-025251/03.  
 XX N-PSDB; AAC90563.  
 XX  
 XX Seventeen nucleic acids encoding PRO polypeptides which are useful in  
 XX diagnosis and treatment of cardiovascular, endothelial or angiogenic  
 XX disorders in a mammal.  
 XX  
 XX Claim 71; Fig 2; 182pp; English.  
 XX  
 XX The present sequence is one of seventeen novel PRO polypeptides. The PRO  
 XX nucleic acids, polypeptides, agonists and antagonists are useful for  
 XX treating cardiovascular, endothelial or angiogenic disorders in a mammal.

CC Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating peridontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder

XX  
SQ Sequence 177 AA;

Query Match 100.0%; Score 951; DB 4; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHRTQGAQRSSWKLFLCSIVMLFLCSFSLIFLFIQLETAKPCMA 60  
Db 1 MCLSHLENMPLSHRTQGAQRSSWKLFLCSIVMLFLCSFSLIFLFIQLETAKPCMA 60

QY 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLFLQNGLYLIYQVAPNANYNDVAFVRLYKN 120  
Db 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLFLQNGLYLIYQVAPNANYNDVAFVRLYKN 120

QY 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLI FNSEHQVLKNTYWGIIILANPQFIS 177  
Db 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLI FNSEHQVLKNTYWGIIILANPQFIS 177

RESULT 8  
AAU81953  
ID AAU81953 standard; protein; 177 AA.  
AC AAU81953;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE Human PRO175.  
XX  
KW Human; PRO; antiinflammatory; ophthalmological; vasotropic;  
KW retinal cell injury; ocular disease; retinitis pigmentosa;  
KW macular degeneration; retinal detachment; retinal tear; retinopathy;  
KW acute retinal degenerative disease; macular hole; degenerative myopia;  
KW Purtscher's retinopathy; oedema; ischaemic condition;  
KW retinal vision occlusion; collagen vascular disease;  
KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Eales disease;  
KW systemic lupus erythematosus; environmental trauma.  
XX  
OS Homo sapiens.  
XX  
PN WO200109327-A2.  
XX  
PD 08-FEB-2001.  
XX  
PF 28-JUL-2000; 2000WO-US020710.  
XX  
PR 28-JUL-1999; 99US-0146222P.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006854.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.

XX (GETH ) GENENTECH INC.  
PA Ashkenazi AJ, Baker KP, Goddard A, Godowski PU, Gurney AL;  
XX Kljavin LJ, Lafleur M, Mark MR, Marsters SA, Pitti RM, Watanabe CK;  
PI Wood WI;  
XX WPI; 2002-130120/17.  
DR N-PSDB; ABK28562.  
XX  
PT Promoting survival of retinal cells, or delaying or preventing retinal  
cell injury or death, by contacting retinal cells with PRO175, 220, 216,  
PT 243, 306, 346, 322, 536, 943, 840, 826, 1068 or PRO1132 polypeptide.  
XX  
PS Claim 44; Fig 2; 152pp; English.  
XX  
CC The invention relates to promoting the survival of retinal cells, or  
delaying or preventing retinal cell injury or death, by contacting the  
CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,  
CC PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO826,  
CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids  
CC encoding the PRO proteins, a vector comprising the nucleic acid, a host  
CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are  
CC useful for promoting survival of retinal cells (retinal neurons such as  
CC retinal ganglion cells, displaced retinal ganglion cells, amacrine cells,  
CC displaced amacrine cells, horizontal neurons or bipolar neurons, rod  
CC photoreceptors, or supportive cells such as Muller cells or pigment  
CC epithelial cells), or delaying or preventing retinal cell injury or death  
CC caused by ocular disease (which is or is associated with retinitis  
CC pigmentosa, macular degeneration, retinal detachment, retinal tear,  
CC retinopathy, retinal degenerative disease, macular hole, degenerative  
CC myopia, acute retinal necrosis syndrome, traumatic chorioretinopathy or  
CC contusion, Purtscher's retinopathy, oedema, an ischaemic condition,  
CC central or branch retinal vision occlusion, collagen vascular disease,  
CC thrombocytopaenic purpura, uveitis, retinal vasculitis, occlusion  
CC associated with Eales disease or systemic lupus erythematosus), retinal  
CC injury or environmental trauma. The retinal cell injury or death is  
CC delayed or prevented by substantially not causing angiogenesis or  
CC mitogenesis. The present sequence represents a PRO protein

XX  
SQ Sequence 177 AA;

Query Match 100.0%; Score 951; DB 5; Length 177;  
Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENMPLSHRTQGAQRSSWKLFLCSIVMLFLCSFSLIFLFIQLETAKPCMA 60  
Db 1 MCLSHLENMPLSHRTQGAQRSSWKLFLCSIVMLFLCSFSLIFLFIQLETAKPCMA 60

QY 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLFLQNGLYLIYQVAPNANYNDVAFVRLYKN 120  
Db 61 KFGPLPSKWQWASSEPCCVKNKVSQWKLFLQNGLYLIYQVAPNANYNDVAFVRLYKN 120

QY 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLI FNSEHQVLKNTYWGIIILANPQFIS 177  
Db 121 KDMIQTLTKSKIQNVGGTYELHVGDTIDLI FNSEHQVLKNTYWGIIILANPQFIS 177

RESULT 9  
ABR42323  
ID ABR42323 standard; protein; 177 AA.  
XX  
AC ABR42323;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Human GITRL protein.  
XX  
KW Human; GITRL; tumour necrosis factor; ligand; cytostatic;  
KW immunomodulator; osteopathic.  
XX  
OS Homo sapiens.

XX WO2003040307-A2.  
XX 15-MAY-2003.  
XX 25-JUL-2002; 2002WO-US023782.  
XX 27-JUL-2001; 2001US-0307838P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Hilbert DH, Rosen CA;  
XX WPI; 2003-430659/40.  
XX N-PSDB; ACC57909.  
XX New heteromultimeric complex having a first polypeptide member of the  
XX tumor necrosis factor (TNF) ligand family, and a second different member  
XX of TNF ligand family, useful for treating cancer, osteoporosis or an  
XX autoimmune disease.  
XX Disclosure; Page 382-383; 388pp; English.  
XX The present sequence is the protein sequence of human GITPL polypeptide.  
XX The invention relates to compositions comprising heterotrimeric complexes  
XX of tumor necrosis factor (TNF) ligand family members, and their use in  
XX the detection, prevention and treatment of disease. In preferred  
XX embodiments, the heterotrimeric complex comprises full-length or  
XX extracellular portions of GITPL together with full-length or  
XX extracellular portions of other TNF ligand family members. The  
XX heterotrimeric complexes of other TNF ligand family members are useful for treating an  
XX autoimmune disease, cancer or osteoporosis, and particularly for  
XX inhibiting cancer cell proliferation, increasing B cell proliferation, or  
XX inducing apoptosis of T cells  
XX Sequence 177 AA;  
XX Query Match 100.0%; Score 951; DB 6; Length 177;  
XX Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MCLSHLENPLSHRTQGAQRSSWKLWLFCSIVMLFLCFSWLIPIFIQLETAKEPCMA 60  
XX 1 MCLSHLENPLSHRTQGAQRSSWKLWLFCSIVMLFLCFSWLIPIFIQLETAKEPCMA 60  
XX 61 KFGPLPSKQWASSEPCVKNKSDWKLKLEILQNGLYLYIGVAPNANNDVAPFEVRLYKN 120  
XX 61 KFGPLPSKQWASSEPCVKNKSDWKLKLEILQNGLYLYIGVAPNANNDVAPFEVRLYKN 120  
XX 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177  
XX 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177  
XX  
XX RESULT 10  
XX ABP60544  
XX ID ABP60544 standard; protein; 177 AA.  
XX AC ABP60544;  
XX DT 28-MAR-2003 (first entry)  
XX  
XX Human tumour necrosis factor endokine-alpha.  
XX  
XX APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta;  
XX dermatological; immunosuppressive; antiinflammatory; antirheumatic;  
XX antiarthritic; cyostatic; antianaemic; antiallergic; antidiabetic;  
XX neuroprotective; ophthalmological; tuberculosic; antidiabetic;  
XX antidiabetic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic;  
XX haemostatic; cancer; autoimmune disease; graft versus host disease; GVHD;  
XX inflammatory disorder; proliferative disorder; single chain antibody;  
XX antibody; human; tumour necrosis factor; endokine-alpha.  
XX

OS Homo sapiens.  
XX WO200294192-A2.  
XX 28-NOV-2002.  
XX 22-MAY-2002; 2002WO-US016106.  
XX 24-MAY-2001; 2001US-0293100P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Ruben SM;  
XX WPI; 2003-156740/15.  
XX Novel isolated antibody that immunospecifically binds tumor necrosis  
XX factor delta, useful for treating, preventing or ameliorating Non-  
XX Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's  
XX syndrome.  
XX Disclosure; Page 214-215; 225pp; English.  
XX The invention relates to a novel antibody or its fragment, which  
XX immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL).  
XX The antibody of the invention has dermatological, immunosuppressive,  
XX antiinflammatory, antirheumatic, antiarthritic, cyostatic, antianaemic,  
XX antiallergic, antidiabetic, neuroprotective, ophthalmological,  
XX tuberculosic, antidiabetic, antiposrotic, anti-HIV,  
XX antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity.  
XX The antibody or its fragment are useful for treating, preventing or  
XX ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in  
XX human, disease or disorder such as autoimmune disease, and graft versus  
XX host disease (GVHD). The autoimmune disease is systemic lupus  
XX erythematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody  
XX is useful for detecting, diagnosing, prognosing, treating, preventing or  
XX ameliorating a disease or disorder associated with aberrant APRIL or  
XX APRIL receptor expression or aberrant function of APRIL or APRIL  
XX receptor. The disease or disorders includes autoimmune and inflammatory  
XX disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis,  
XX asthma, allergic encephalomyelitis, myocarditis, multiple sclerosis,  
XX uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune  
XX system, particularly B cell cancers, immune disorders such as myasthenia  
XX gravis, Hashimoto's disease, immunodeficiency syndrome, Bruton's disease,  
XX infectious diseases (e.g. acquired immunodeficiency syndrome (AIDS)), and  
XX proliferative disorders (e.g. leukemia). The present sequence represents  
XX the tumour necrosis factor endokine-alpha  
XX Sequence 177 AA;  
XX Query Match 100.0%; Score 951; DB 6; Length 177;  
XX Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
XX Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 MCLSHLENPLSHRTQGAQRSSWKLWLFCSIVMLFLCFSWLIPIFIQLETAKEPCMA 60  
XX 1 MCLSHLENPLSHRTQGAQRSSWKLWLFCSIVMLFLCFSWLIPIFIQLETAKEPCMA 60  
XX 61 KFGPLPSKQWASSEPCVKNKSDWKLKLEILQNGLYLYIGVAPNANNDVAPFEVRLYKN 120  
XX 61 KFGPLPSKQWASSEPCVKNKSDWKLKLEILQNGLYLYIGVAPNANNDVAPFEVRLYKN 120  
XX 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177  
XX 121 KDMIQTLTNKSKIQNVGGTYELHVGDTIDLIFNSEHQVLKNTYWGIIILLANPQFIS 177  
XX  
XX RESULT 11  
XX ADC35222  
XX ID ADC35222 standard; protein; 177 AA.  
XX AC ADC35222;  
XX

DT 18-DEC-2003 (first entry)  
 XX Human TNF ligand family member #20.  
 DE human; tumour necrosis factor; TNF ligand; endokine alpha;  
 XX excessive bone resorption disorder; osteoporosis; Paget's disease;  
 KW arterial calcification.  
 KW Homo sapiens.  
 XX US2003100074-A1.  
 PN 29-MAY-2003.  
 XX 15-AUG-2002; 2002US-00218547.  
 XX 16-AUG-2001; 2001US-0312542P.  
 PR 30-OCT-2001; 2001US-0330761P.  
 XX (YUGG/) YU G.  
 PA (NIJ/) NI J.  
 PA (ROSE/) ROSEN C A.  
 PA (NARD/) NARDELLI B.  
 XX Yu G, Ni J, Rosen CA, Nardelli B;  
 PI WPI; 2003-696072/66.  
 DR N-PSDB; ADC35221.  
 XX New Endokine alpha gene useful for preparing a composition for treating a  
 PT disease associated with excessive or insufficient bone resorption e.g.,  
 PT osteoporosis, Paget's disease or arterial calcification.  
 XX Claim 1; SEQ ID NO 40; 145pp; English.  
 PS The invention relates to an isolated nucleic acid molecule encoding a  
 CC tumour necrosis factor family ligand. A composition comprising the  
 CC isolated antibody or its fragment is used for treating an individual in  
 CC need of decreased level of endokine alpha activity. The endokine alpha  
 CC polypeptide present in a heterotrimeric complex is used for treating an  
 CC individual having a disorder associated with excessive bone resorption,  
 CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an  
 CC individual having a disorder associated with insufficient bone resorption  
 CC comprises administering an endokine alpha antagonist, which is the  
 CC antibody that binds specifically to endokine alpha polypeptide. The  
 CC present sequence represents the amino acid sequence of a tumour necrosis  
 CC factor family ligand.  
 XX Sequence 177 AA;  
 SQ Query Match 100.0%; Score 951; DB 7; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-97;  
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MCLSHLENPLSHRSTQGAQRSSWKLWFLCSIVMLFLCSFSLFIPIQLTAKEPCMA 60  
 DB 1 MCLSHLENPLSHRSTQGAQRSSWKLWFLCSIVMLFLCSFSLFIPIQLTAKEPCMA 60  
 QY 61 KFGPLPSKWQMASSEPPCVNKVSDWKLKILQNGLYLYGVAPNANYNVDVAFVRLYKN 120  
 DB 61 KFGPLPSKWQMASSEPPCVNKVSDWKLKILQNGLYLYGVAPNANYNVDVAFVRLYKN 120  
 QY 121 KDMIQTLTKSKIQNVGGTYVELHVGDTIDLFNFSHQVILKNNTYGIILLANPQFIS 177  
 DB 121 KDMIQTLTKSKIQNVGGTYVELHVGDTIDLFNFSHQVILKNNTYGIILLANPQFIS 177  
 RESULT 12  
 AAW37847  
 ID AAW37847 standard; protein; 169 AA.  
 XX AAW37847;  
 AC  
 XX

DT 28-AUG-1998 (first entry)  
 XX Human endokine-alpha.  
 DE Endokine-alpha; cytokine; tumour necrosis factor; human;  
 KW immunomodulation; infection; cell proliferation; angiogenesis; tumour;  
 KW metastasis; apoptosis; sepsis; endotoxaemia; melanoma; sarcoma;  
 KW diagnosis; therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Domain 1..17 /note= "intracellular domain"  
 FT Domain 18..43 /note= "transmembrane domain"  
 FT Domain 44..169 /note= "extracellular domain"  
 FT Peptide 44..158 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 44..54 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 57..68 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 69..78 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 94..105 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 108..132 /note= "epitope-bearing fragment (Claim 13)"  
 FT Peptide 142..158 /note= "epitope-bearing fragment (Claim 13)"  
 XX PN WO9807880-A1.  
 XX PD 26-FEB-1998.  
 XX 16-AUG-1996; 96WO-US013282.  
 PR 16-AUG-1996; 96WO-US013282.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Yu G, Ni J, Rosen CA;  
 XX WPI; 1998-169182/15.  
 DR N-PSDB; AAV19195.  
 XX Nucleic acid encoding human endokine-alpha - useful for diagnosis and  
 treatment of tumour necrosis factor-related diseases.  
 Claim 1; Fig 1A-B; 78pp; English.  
 This polypeptide comprises human endokine-alpha, a novel member of the  
 tumour necrosis factor (TNF) family of cytokines that shows 30%  
 similarity and 22% identity to human TNF-alpha. Its amino acid sequence  
 was deduced from a human striatum cDNA clone (see AAV19195). Isolation of  
 this nucleic acid allows production of recombinant endokine-alpha  
 polypeptides in transformed host cells. Endokine-alpha may be involved in  
 disorders of immunomodulation, infection, cell proliferation,  
 angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia, and  
 may be useful for treating melanoma and sarcoma, particularly where  
 coupled to a radioisotope or cytostatic agent. Antibodies raised against  
 endokine-alpha are useful diagnostically and for treatment of TNF-  
 associated disease  
 XX Sequence 169 AA;  
 SQ Query Match 95.3%; Score 906; DB 2; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-92;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 MPLSHRTQGAQRSSWKLWFLCSIVMLFLCSFSLFIPIQLTAKEPCMAKFGPLPSK 68

```

Db 1 MPLSHSRTQGAORSSWKLFCSIVMLLFLCSFWLFIQLQETAKPCWAKFGPLPSK 60
QY 69 WQVASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPFVRLYKKNKDMIQTLT 128
Db 61 WQVASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPFVRLYKKNKDMIQTLT 120
QY 129 NKSQIONVGGTYELHVGDTIDLFNSEHQLKNTYWGIIILANPQFIS 177
Db 121 NKSQIONVGGTYELHVGDTIDLFNSEHQLKNTYWGIIILANPQFIS 169

RESULT 13
AAB08785
ID AAB08785 standard; protein; 169 AA.
XX
AC AAB08785;
XX
DT 02-JAN-2001 (first entry)
XX
DE A human endokine-alpha polypeptide.
XX
KW Human; endokine-alpha; cytokine; tumour necrosis factor; TNF; AIDS;
KW chronic lymphocyte disorder; tumour; parasitic disease; arthritis;
KW autoimmune disease; lupus; multiple sclerosis; chronic inflammation;
KW acute inflammation; acute allograft rejection; graft versus host disease;
KW transplant rejection; foetal resorption; faecal peritonitis; allergy;
KW bowel disease; sepsis; leukaemia; chronic hypergammaglobulinemia;
KW polychondritis; scleroderma; Wegener granulomatosis; dermatomyositis;
KW chronic active hepatitis; myasthenia gravis; psoriasis; vitiligo;
KW Steven-Johnson syndrome; idiopathic sprue; gluten-sensitive enteropathy;
KW pemphigus vulgaris; Goodpasture's disease; bullous pemphigoid;
KW discoid lupus; dense deposit disease; endocrine ophthalmopathy;
KW irritable bowel disease; asthma; Grave's disease; sarcoidosis; cirrhosis;
KW juvenile diabetes; insulin dependent diabetes mellitus; uveitis;
KW lymphopenias; polyarteritis nodosa; Sjogren's syndrome; Bechet's disease;
KW primary myxedema; polymyositis; mixed connective tissue disease;
KW keratoconjunctivitis sicca; vernal keratoconjunctivitis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..17 /note= "intracellular domain"
FT Domain 18..43 /note= "transmembrane domain"
FT Domain 44..169 /note= "extracellular domain"
XX
W0200050620-A2.
XX
PD 31-AUG-2000.
XX
XX 25-FEB-2000; 2000WO-US004722.
XX
XX 26-FEB-1999; 99US-0122099P.
XX
XX 28-MAY-1999; 99US-0136788P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Yu G, Ni J, Rosen CA;
XX
XX WPI; 2000-572097/53.
XX
XX N-PSDB; AAA74936.
XX
XX Polynucleotide encoding endokine alpha protein, which is a member of
XX tumor necrosis factor useful for treating inflammatory diseases,
XX disorders such as cancer, allergy, diabetes and various neurological
XX disorders.
XX
XX Claim 16; Fig 1; 263pp; English.
XX
XX The present sequence represents a human endokine-alpha polypeptide. The

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CC polypeptide is a cytokine which is similar to tumour necrosis factor
CC (TNF). The endokine-alpha polynucleotides and polypeptides are useful for
CC treating AIDS, chronic lymphocyte disorder, tumours, parasitic disease,
CC autoimmune disease, lupus, arthritis, multiple sclerosis, chronic
CC inflammation, acute inflammation, acute allograft rejection, graft versus
CC host disease, transplant rejection, foetal resorption, faecal
CC peritonitis, skin allergies, bowel disease, sepsis, leukaemia, chronic
CC hypergammaglobulinemia, polychondritis, scleroderma, Wegener
CC granulomatosis, dermatomyositis, chronic active hepatitis, myasthenia
CC gravis, psoriasis, Steven-Johnson syndrome, idiopathic sprue, vitiligo,
CC gluten-sensitive enteropathy, pemphigus vulgaris, Goodpasture's disease,
CC bullous pemphigoid, discoid lupus, dense deposit disease, endocrine
CC ophthalmopathy, irritable bowel disease, asthma, Grave's disease,
CC sarcoidosis, cirrhosis, juvenile diabetes, insulin dependent diabetes
CC mellitus, uveitis, lymphopenias, polyarteritis nodosa, Sjogren's
CC syndrome, Bechet's disease, primary myxedema, polymyositis, mixed
CC connective tissue disease, keratoconjunctivitis sicca, and vernal
CC keratoconjunctivitis,
XX
SQ Sequence 169 AA;

Query Match 95.3%; Score 906; DB 3; Length 169;
Best Local Similarity 100.0%; Pred. NO. 3.6e-92;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MPLSHSRTQGAORSSWKLFCSIVMLLFLCSFWLFIQLQETAKPCWAKFGPLPSK 68
Db 1 MPLSHSRTQGAORSSWKLFCSIVMLLFLCSFWLFIQLQETAKPCWAKFGPLPSK 60
QY 69 WQVASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPFVRLYKKNKDMIQTLT 128
Db 61 WQVASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPFVRLYKKNKDMIQTLT 120
QY 129 NKSQIONVGGTYELHVGDTIDLFNSEHQLKNTYWGIIILANPQFIS 177
Db 121 NKSQIONVGGTYELHVGDTIDLFNSEHQLKNTYWGIIILANPQFIS 169

RESULT 14
AAY53061
ID AAY53061 standard; protein; 169 AA.
XX
AC AAY53061;
XX
DT 03-APR-2000 (first entry)
XX
DE Human endokine alpha protein SEQ ID NO:2.
XX
KW Human; endokine alpha; tumour necrosis factor; TNF; cytokine;
KW immunomodulation; inflammation; cell proliferation; angiogenesis;
KW tumour metastasis; apoptosis; sepsis; endotoxemia.
XX
OS Homo sapiens.
XX
XX US9998171-A.
XX
PD 07-DEC-1999.
XX
XX 15-AUG-1997; 97US-00912227.
XX
XX 16-AUG-1996; 96US-0024058P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ni J, Rosen CA, Yu G;
XX
XX WPI, 2000-104608/09.
XX
XX N-PSDB; AAZ57314.
XX
XX Isolated human endokine alpha gene useful as a diagnostic probes and
XX primers.
XX
XX Claim 1; Fig 1; 31pp; English.

```

XX CC The present sequence represents human endokine alpha which is a member of  
 CC the tumour necrosis factor (TNF) family of cytokines. Endokine alpha  
 CC protein and polynucleotides can be used in diagnostic and therapeutic  
 CC methods concerning TNF family-related disorders. These include disorders  
 CC associated with immunomodulation and inflammation, cell proliferation,  
 CC angiogenesis, tumour metastasis, apoptosis, sepsis and endotoxaemia  
 XX Sequence 169 AA;

Query Match 95.3%; Score 906; DB 3; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-92;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 MPLSHRTQGAQRSSWKLWFLCSIVMLFLCSFSLIFLQLETAKEPCMAKFGPLPSK 58  
 Db 1 MPLSHRTQGAQRSSWKLWFLCSIVMLFLCSFSLIFLQLETAKEPCMAKFGPLPSK 60  
 QY 69 WQMASSEPPCVNKVSDWKLILQNGLYLIYQVAPNANYNDVAPFEVRLYKNDMIQTILT 128  
 Db 61 WQMASSEPPCVNKVSDWKLILQNGLYLIYQVAPNANYNDVAPFEVRLYKNDMIQTILT 120  
 QY 129 NKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGILLANPOFIS 177  
 Db 121 NKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGILLANPOFIS 169

RESULT 15  
 ADA11464  
 ID ADA11464 standard; protein; 169 AA.  
 AC ADA11464;  
 XX 06-NOV-2003 (first entry)  
 XX Human endokine alpha.

XX human, endokine alpha; melanoma; sarcoma; tumour; tumour regression;  
 KW infection; viral; bacterial; yeast; fungal; Toxoplasma gondii;  
 KW Schistosoma mansoni; Listeria monocytogenes; tumour necrosis factor;  
 KW TNF-related disorder; endokine alpha-related disorder; immunomodulation;  
 KW inflammation; cell proliferation; angiogenesis; tumour metastasis;  
 KW apoptosis; sepsis; endotoxaemia.  
 XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Domain 1..17  
 FT Domain /label = Intracellular\_domain  
 FT Domain 18..43  
 FT Domain /label = Transmembrane\_domain  
 FT Domain 44..169  
 FT Domain /label = Extracellular\_domain  
 XX US2002099198-A1.  
 XX 25-JUL-2002.  
 XX 01-JUL-1999; 99US-00345790.  
 XX 16-AUG-1996; 96US-0024058P.  
 XX 15-AUG-1997; 97US-00912227.  
 XX (YUGG/) YU G.  
 XX (NLJJ/) NI J.  
 XX (ROSE/) ROSEN C A.  
 XX Yu G, Ni J, Rosen CA;  
 XX WPI; 2003-605663/57.  
 XX N-PSDB; ADA11463.

XX Novel isolated endokine alpha polypeptide, a member of tumor necrosis

PT factor ligand family, and antibodies against the polypeptides, useful for  
 PT treating melanoma, sarcoma, and viral, bacterial, fungal infections.  
 XX Claim 16; Fig 1; 29pp; English.

CC The invention relates to an isolated human endokine alpha polypeptide. A  
 CC cell recombinant for the human endokine alpha polypeptide is useful for  
 CC producing the protein by recombinant techniques. The antigenic epitope  
 CC bearing peptides and polypeptides are useful to raise antibodies  
 CC including monoclonal antibodies. The peptides and antipeptide antibodies  
 CC are used in a variety of qualitative or quantitative assays for the  
 CC protein. The protein is useful for tumour targeting and thus used in  
 CC patients with melanoma and sarcoma for tumour regression and extension of  
 CC patient life-span through a local injection. The protein is also useful  
 CC for treating viral, bacterial, yeast, fungal and other infections e.g.,  
 CC Toxoplasma gondii, Schistosoma mansoni, Listeria monocytogenes etc. The  
 CC protein is also useful for treating other tumour necrosis factor (TNF)-  
 CC related disorders. The nucleic acid is useful as probes for gene mapping  
 CC by in situ hybridisation and for detecting expression of endokine alpha  
 CC gene in human tissue e.g. by Northern blot analysis. The nucleic acid is  
 CC also useful for diagnosing an endokine alpha-related disorder such as  
 CC disorders associated with immunomodulation and inflammation, cell  
 CC proliferation, angiogenesis, tumour metastasis, apoptosis, sepsis or  
 CC endotoxaemia. The antibody is useful diagnostically or therapeutically as  
 CC antagonists in the treatment of alpha and/or TNF-related disorders. The  
 CC antibody is also useful for purification of the protein. The antibodies  
 CC are useful for detecting the protein and for tracking the fate of various  
 CC regions of a protein precursor which undergoes post-translational  
 CC processing. The present sequence represents the amino acid sequence of  
 CC human endokine alpha.

XX Sequence 169 AA;

Query Match 95.3%; Score 906; DB 6; Length 169;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-92;  
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 MPLSHRTQGAQRSSWKLWFLCSIVMLFLCSFSLIFLQLETAKEPCMAKFGPLPSK 58  
 Db 1 MPLSHRTQGAQRSSWKLWFLCSIVMLFLCSFSLIFLQLETAKEPCMAKFGPLPSK 60  
 QY 69 WQMASSEPPCVNKVSDWKLILQNGLYLIYQVAPNANYNDVAPFEVRLYKNDMIQTILT 128  
 Db 61 WQMASSEPPCVNKVSDWKLILQNGLYLIYQVAPNANYNDVAPFEVRLYKNDMIQTILT 120  
 QY 129 NKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGILLANPOFIS 177  
 Db 121 NKSKIQNVGGTYELHVGDTIDLIENSEHQVLKNTYWGILLANPOFIS 169

Search completed: April 8, 2004, 14:46:07  
 Job time : 52 secs



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OM protein - protein search, using sw model

Run on: April 8, 2004, 14:44:53 ; Search time 23 Seconds  
(without alignments)  
397.296 Million cell updates/sec

Title: US-09-613-972A-14  
Perfect score: 951  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/2/iaa/5B COMB.pcp.\*  
3: /cgn2\_6/prodata/2/iaa/6A COMB.pcp.\*  
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5: /cgn2\_6/prodata/2/iaa/6C COMB.pcp.\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906	95.3	169	2	US-08-912-227-2
2	906	95.3	169	2	Sequence 2, Appli
3	906	95.3	169	2	Sequence 2, Appli
4	84.5	8.9	1221	4	US-09-345-790-2
5	77	8.1	326	3	Sequence 3959, Ap
6	77	8.1	326	6	Patent No. 5395759
7	77	8.1	2763	3	US-08-496-944-2
8	75.5	7.9	550	3	Sequence 9, Appli
9	75	7.9	325	4	Sequence 5760, Ap
10	74.5	7.8	271	4	Sequence 33, Appli
11	74.5	7.8	543	3	Sequence 2, Appli
12	74.5	7.8	543	3	Sequence 2, Appli
13	74	7.8	157	5	PCT-US93-02475-6
14	74	7.8	567	4	US-09-645-926A-7
15	73.5	7.7	609	4	US-09-396-149-6
16	73	7.7	166	3	US-08-765-381-12
17	71.5	7.5	233	1	US-08-323-445A-10
18	71.5	7.5	233	1	US-08-515-903A-10
19	71.5	7.5	233	2	US-08-512-227-3
20	71.5	7.5	233	2	US-08-330-088B-2
21	71.5	7.5	233	3	US-08-883-086-6
22	71.5	7.5	233	3	US-08-880-342-37
23	71.5	7.5	233	4	US-09-589-287B-3
24	71.5	7.5	233	4	US-09-513-584-3
25	71.5	7.5	233	4	US-09-157-864-9
26	71.5	7.5	233	4	US-10-082-260-5
27	71.5	7.5	233	4	US-09-345-790-3

28 71.5 7.5 233 4 US-09-982-308B-22 Sequence 22, Appli  
29 71.5 7.5 233 4 US-09-879-919-5 Sequence 5, Appli  
30 71.5 7.5 233 4 US-09-588-947A-3 Sequence 3, Appli  
31 71.5 7.5 233 4 US-09-131-237C-3 Sequence 3, Appli  
32 71.5 7.5 233 4 US-09-589-386A-3 Sequence 3, Appli  
33 71.5 7.5 233 5 PCT-US93-12840-10 Sequence 10, Appli  
34 71.5 7.5 233 6 5422425-2 Patent No. 5422425  
35 71.5 7.5 693 3 US-08-960-048-11 Sequence 11, Appli  
36 71.5 7.5 693 3 US-09-838-586-11 Sequence 11, Appli  
37 71 7.5 157 5 PCT-US93-02475-2 Sequence 2, Appli  
38 71 7.5 1082 1 US-08-106-493A-2 Sequence 2, Appli  
39 71 7.5 1082 1 US-08-429-264-2 Sequence 2, Appli  
40 70 7.4 157 5 PCT-US93-02475-7 Sequence 7, Appli  
41 70 7.4 1139 1 US-08-832-883-2 Sequence 2, Appli  
42 70 7.4 1139 2 US-08-832-877-2 Sequence 2, Appli  
43 69.5 7.3 211 4 US-09-322-409-78 Sequence 78, Appli  
44 69.5 7.3 211 4 US-09-451-527-78 Sequence 78, Appli  
45 69.5 7.3 217 4 US-09-489-039A-8076 Sequence 8076, Ap

ALIGNMENTS

RESULT 1  
US-08-912-227-2  
; Sequence 2, Application US/08912227  
; Patent No. 5996171  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912,227  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,058  
; FILING DATE: 16-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-912-227-2

Query Match 95.3%; Score 906; DB 2; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.3e-99;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 MPLSHSTQGAQRSSWKWLFCSFVWLFIFLOLETAKEPCWAKFGPLPSK 68  
|||||

Db 1 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCFSFWLFIQLETAKEPCMAKFGPLPSK 60  
Qy 69 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 128  
Db 61 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 120  
Qy 129 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 177  
Db 121 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 169

RESULT 2  
US-09-513-584-2  
; Sequence 2, Application US/09513584  
; Patent No. 640867  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha and Methods  
; TITLE OF INVENTION: of Use  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,  
; ADDRESSEE: P.L.L.C  
; STREET: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/513,584  
; FILING DATE: 25-FEB-2000  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/024,058  
; FILING DATE: 16-AUG-1996  
; PRIOR APPLICATION DATA: US 60/912,227  
; APPLICATION NUMBER: US 60/122,099  
; FILING DATE: 26-FEB-1999  
; PRIOR APPLICATION DATA: US 60/136,788  
; APPLICATION NUMBER: US 60/136,788  
; FILING DATE: 28-MAY-1999  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 09/345,790  
; FILING DATE: 01-JUL-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-513-584-2

Query Match 95.3%; Score 906; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.3e-99;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCFSFWLFIQLETAKEPCMAKFGPLPSK 68  
Db 1 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCFSFWLFIQLETAKEPCMAKFGPLPSK 60  
Qy 69 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 128  
Db 61 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 120  
Qy 129 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 177  
Db 121 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 169

RESULT 3  
US-09-345-790-2  
; Sequence 2, Application US/09345790  
; Patent No. 6521742  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang  
; APPLICANT: Ni, Jian  
; APPLICANT: Rosen, Craig A.  
; TITLE OF INVENTION: Human Endokine Alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C  
; ADDRESSEE: 1100 NEW YORK AVE., NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/345,790  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/912,227  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Steffe, Eric K.  
; REGISTRATION NUMBER: 36,688  
; REFERENCE/DOCKET NUMBER: 1488.0470001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 169 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-345-790-2

Query Match 95.3%; Score 906; DB 4; Length 169;  
Best Local Similarity 100.0%; Pred. No. 2.3e-99;  
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCFSFWLFIQLETAKEPCMAKFGPLPSK 68  
Db 1 MPLSHRTQGAQRSSWKLWLFCSIVMLLFLCFSFWLFIQLETAKEPCMAKFGPLPSK 60  
Qy 69 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 128  
Db 61 WQMASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANYNDVAPFEVRLYKNDMIQTLT 120  
Qy 129 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 177  
Db 121 NKSKIQNVGGTYELHVGDTIDILFNSEHQLVKNNTYWGIIILLANPOFIS 169



5395759-2

Query Match 8.1%; Score 77; DB 6; Length 326;  
Best Local Similarity 22.8%; Pred. No. 1.2;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LNLFCSTVMLLFLC-----SFSWLIIFLQLETAKEPCMAK-----FGPLSKWQM 71  
DB 10 LTLISILLNYLKITNTMDIIFRLLLIALLISFVFTQYNGMYLPTGSLDAVYN 69  
QY 72 ASSEPP-----CV-----NKVSDWKLEILQNGLYIGQVAPNA---NTNDVAPFEV 115  
DB 70 STSGEPPLTCLGYPAEAKNEISDDEMENTLSQLFLTKGWPIGVSFYFKYNDINTFSV 129  
QY 116 --RLYKNDMLQTLNKSQKQNGVGGIYELHVGDTIDLIENSEHVLKNNYNGIILLANP 173  
DB 130 NPQLYCDYNVV-----LMRYDNTSELDASELADLIINE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171

## RESULT 7

US-08-496-944-2  
; Sequence 2, Application US/08496944  
; Patent No. 6040496  
; GENERAL INFORMATION:  
; APPLICANT: Law, Marcus D  
; APPLICANT: Dietz, Jon M  
; TITLE OF INVENTION: Use of Translationally altered RNA to  
; TITLE OF INVENTION: Confer Resistance to Maize Dwarf Mosaic Virus and Other  
; TITLE OF INVENTION: Monocotyledonous Plant Viruses  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CIBA-Geigy Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10532  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30B  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/496,944  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott  
; REGISTRATION NUMBER: 36,129  
; REFERENCE/DOCKET NUMBER: CGC 1814  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2763 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-496-944-2

Query Match 8.1%; Score 77; DB 3; Length 2763;  
Best Local Similarity 25.0%; Pred. No. 30;  
Matches 31; Conservative 20; Mismatches 53; Indels 20; Gaps 5;  
QY 51 LETAKEPCMAKFGPLPSKWQVASEPCCVKNVSKWLEILQNGLYIGQVAPNANNDV 110  
DB 18 IQFKERCNPKFSLHPLTQVAETIGHYTDNQSKQIMDV-SEALIKVNTLTTPDDAKASA 76  
QY 111 APFEV-RLYKNN-----DMQTLNKSQKQNGVGGIYELHVGDTIDLIENSEHVLKNN-N 162  
DB 77 ALLEVSRYKNNKSKSLKTSLESFRNK-----ISPKSTINAAALMCDNQDNKNN 125

QY 163 TYWG 166  
DB 126 FWG 129

## RESULT 8

US-09-039-859-9  
; Sequence 9, Application US/09039859  
; Patent No. 6063987  
; GENERAL INFORMATION:  
; APPLICANT: Daub, Margaret E.  
; APPLICANT: Ehrenshaft, Marilyn  
; APPLICANT: Jenns, Ann E.  
; TITLE OF INVENTION: Isolated Genes and Proteins Encoding  
; TITLE OF INVENTION: Resistance to Photosensitizers  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Virginia C. Bennett  
; STREET: PO Box 37428  
; CITY: Raleigh  
; STATE: No 6063987th Carolina  
; COUNTRY: US  
; ZIP: 27627  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/039,859  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bennett, Virginia C.  
; REGISTRATION NUMBER: 37,092  
; REFERENCE/DOCKET NUMBER: 5405.333  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-854-1400  
; TELEFAX: 919-854-1401  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 550 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-039-859-9

Query Match 7.9%; Score 75.5; DB 3; Length 550;  
Best Local Similarity 18.5%; Pred. No. 4;  
Matches 43; Conservative 33; Mismatches 55; Indels 101; Gaps 13;  
QY 12 SHSRTOGAQRSSKWLFPC---SIVMLLFL---CSFSWLIIFLQLETAKEPCMAKFGPL 65  
DB 188 SYESVEG-----WRAWLGCHVLSVMAIFMRKSMTASWT---EQHEQAR--LMLQYSPL 236  
QY 66 ---PSKW-----QMASSEP---PCVKNVSKWLEI- 89  
DB 237 NADSDRWLAQYIRABRLCEEVSEQVDLTNTSFYRDVADPATENPVQTCRNKILNWKMGVP 296  
QY 90 ---LQNGLYLIGQVAPNANNDVAPFEVLLYKNDMIOTLTNKSQI-----133  
DB 297 QALRSPLIMFWEHVA-----TAYMHBEVLTAATNKSFTAPYLAERLSLTDF 343  
QY 134 -----QNVGGTYEL--HVGDTIDLIENSEHVLKNNYNGIILLANPQFI 176  
DB 344 PFLVTDQTHITAVYELTAQVQLDIFINYDTK-----SLVASPSLV 385

## RESULT 9

US-09-328-352-S760  
; Sequence 5760, Application US/09328352  
; Patent No. 6562958

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/ GENERAL INFORMATION:
/ APPLICANT: GARY L. Breton et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
/ TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC99-03PA
/ CURRENT APPLICATION NUMBER: US/09/328,352
/ CURRENT FILING DATE: 1999-06-04
/ NUMBER OF SEQ ID NOS: 5252
/ SEQ ID NO 5760
/ LENGTH: 325
/ TYPE: PRT
/ ORGANISM: Acinetobacter baumannii
/ US-09-328-352-5760

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[illegible]

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RESULT 10
US-09-443-041A-33
; Sequence 33, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443, 041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-09-443-041A-33

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Query Match      7.8%; Score 74.5; DB 4; Length 271;
Best Local Similarity 22.7%; Pred. No.1.8;
Matches 34; Conservative 23; Mismatches 50; Indels 43; Gaps 9;

Qy 10 PLSHSRTGQGRSSWKWL--FCISVMLFLFCSPSLIFIF----- 48
Db 31 PLPH-MLQG-----WLRNYIGVLLYFISGFLMCFYIYHLKRNVIYKDALPSNKAM 81
Qy 49 -LQLETAKEPCWAKFGPLP--SKQWASSEPCCVNVKUSD--WKLEILQNGLYLI---YQG 100
Db 82 LLOISVAMK-ANPYCALPSPSEYMIENGWTKCARISDVGLSVIYAAILYVIVEFGI 140
Qy 101 VAPNANTYNDVAPFEVRLYKNDMTQTLTNK 130
Db 141 YWMHMLHDIKP----LYKYLHATHIYNK 166

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RESULT 11  
US-08-697-610-2

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; Sequence 2, Application US/08697610
; Patent No. 6172187
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: CD40 Associated Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,610
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/349,357
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: F-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-697-610-2

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Query Match	7.8%	Score	74.5	DB	3	Length	543
Best Local Similarity	25.5%	Pred. No.	5.2				
Matches	36	Conservative	20	Mismatches	42	Indels	43
						Gaps	8
Qy	30	CSIVMLFLCFSKLI	FIPLQLETAKEPCMAKFGPLPSKQWMASEP	PCVKNVSDW	---	---	85
Db	199	CVWVSCPHKCSQVLT	---	LRSEGTNQIKA	-----	HEASAVOHVLLKEWNSL	245
Qy	86	--KLEILLONGLIYGVQAPNAN	---	YNDVAPFEVRLYKNDKI	QTLTKNSKIQNVGGT	139	
Db	246	EKVYSLQN	-----	ESVEKNKS	QSLHNLQICSFEIERQKEMLR	---NNESKI	291
Qy	140	YELHVGDTIDILFNSEHQVLK	160				
Db	292	--LHLORVID	---	--SQAEKLK	306		

RESULT 12  
US-08-349-357-2  
; Sequence 2, Application US/08349357  
; Patent No. 6265556  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Sato, Takasaki  
; TITLE OF INVENTION: C940 Associated Proteins  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA

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; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,357
; FILING DATE: 02-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 543 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-349-357-2

Query Match 7.8%; Score 74.5; DB 3; Length 543;
Best Local Similarity 25.5%; Pred. No. 5.2;
Matches 36; Conservative 20; Mismatches 42; Indels 43; Gaps 8;

QY 30 CSIVMLFLCSFSLWLIFFIQLETAKEPCWAKFGPLPSKQWMASSBPPCVNKVSDW----- 85
DB 199 CVVYSCPKSCVQTL-----LRSEGTNQIKA-----HEASSAVQHVNLKWSNSL 245
QY 86 --KLEIIIONGLYLYIGVQVAPNAN---YNDVAPFEVRLYKNDMIQTLTKNSKIQNVGGT 139
DB 246 EKVSLQN-----ESVEKNKQSLHNQICSFIEIERQKMLR--NNESKI----- 291
QY 140 YELHVGDTIDLPNSEHVLK 160
DB 292 --LHLQVID-----SQAEK 306

RESULT 13
PCT-US93-02475-6
; Sequence 6, Application PC/TUS9302475
; GENERAL INFORMATION:
; APPLICANT: Wisnieski, Bernadine J.
; TITLE OF INVENTION: Tumor Necrosis Factor with Modified
; TITLE OF INVENTION: Ion Channel
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Donald G. Lewis
; STREET: 8328 Regents Road #1E
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 M storage
; COMPUTER: VE System 386
; OPERATING SYSTEM: MS-DOS 5
; SOFTWARE: Word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02475
; FILING DATE: 19930412
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 07/852,625
; FILING DATE: 12 March 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Donald G. Lewis
; REGISTRATION NUMBER: 28636
; REFERENCE/DOCKET NUMBER: BUW-2

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 554-2421
; TELEFAX: (619) 554-6312
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: AMINO ACIDS
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Tumor Necrosis Factor (feline)
; PUBLICATION INFORMATION:
; AUTHORS: McGraw, R. A., Coffee, B.W., Otto,
; AUTHORS: C.M., Drews, R.T. and Rawling, C.A.
; TITLE: Gene Sequence of Feline Tumor Necrosis
; TITLE: Factor
; JOURNAL: Nucleic Acids Research
; VOLUME: 18
; PAGES: 5564
; DATE: 1990
; RELEVANT RESIDUES IN SEQ ID NO: 6: 1-157
; PCT-US93-02475-6

Query Match 7.8%; Score 74; DB 5; Length 157;
Best Local Similarity 24.4%; Pred. No. 0.92;
Matches 30; Conservative 21; Mismatches 32; Indels 40; Gaps 6;

QY 81 KVSQWKLEIIIONGLYLYIGVQV-----APNANY---NDVAPFEVRLYKNDMIQTLTKNS 131
DB 42 ELTDNQLKVPDGLYLYISQVLTFTGCGCPSTHLLTHAISRAFSYQTKVNLISAI--XS 99
QY 132 KIQN-----YGGTYELHVGDTID-----LIFNSEHVLKNTYWG 167
DB 100 PQCRETPEGAEPKPYEPIYLGVGVFQLEKGRDLSTELNPAYLDFAESGV-----YFGI 154
QY 168 ILL 170
DB 155 IAL 157

RESULT 14
US-09-645-926A-7
; Sequence 7, Application US/09645926A
; Patent No. 6482411
; GENERAL INFORMATION:
; APPLICANT: AHUJA, SEEMA
; APPLICANT: BONEWALD, LYNDIA
; TITLE OF INVENTION: CD40 LIGAND AND CD40 AGONIST COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: 4003.001000
; CURRENT APPLICATION NUMBER: US/09/645,926A
; CURRENT FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/151,250
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 7
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-645-926A-7

Query Match 7.8%; Score 74; DB 4; Length 567;
Best Local Similarity 28.3%; Pred. No. 6.3;
Matches 28; Conservative 17; Mismatches 24; Indels 30; Gaps 6;

QY 72 ASSEPPCVNKVSDW-----KLEIIIONGLYLYIGVQVAPNAN---YNDVAPFEVRLYK 121
DB 252 ASSAVQHVNLKWSNSLEKVSLLQN-----ESVEKNKQSLHNQICSFIEIERQK 305
QY 122 DMIQTLTKNSKIQNVGGTYELHVGDTIDLPNSEHVLK 160
DB 306 EMLR--NNESKI-----LHLQVID-----SQAEK 330

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 8, 2004, 14:44:52 ; Search time 18 Seconds  
(without alignments)  
512.023 Million cell updates/sec

Title: US-09-613-972A-14

Perfect score: 951

Sequence: 1 MCLSHLENPLSHRSRTQGAQ.....VLKNTYWGILLANPQFIS 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	951	100.0	177	1	TN18 HUMAN
2	108.5	11.4	272	1	TNF5 CHICK
3	85.5	9.0	377	1	MCL1 HUMAN
4	79	8.3	372	1	PROB OCEAN
5	78	8.2	564	1	Y61A MYCPN
6	77.5	8.1	233	1	TNFA FELCA
7	77.5	8.1	880	1	ARG2 YEAST
8	77.5	8.1	3584	1	NBEA DROME
9	77	8.1	326	1	VS09 ROTH
10	77	8.1	326	1	VS09 ROTH
11	77	8.1	326	1	VS09 ROTH
12	76.5	8.0	233	1	TNFA PAPHU
13	75	7.9	129	1	V061 FOWPV
14	74.5	7.8	233	1	TNFA PAPSP
15	74.5	7.8	271	1	SCSD TOBAC
16	74.5	7.8	354	1	GBI HOMAM
17	74	7.8	567	1	TRA3 MOUSE
18	74	7.8	568	1	TRA3 HUMAN
19	73.5	7.7	609	1	RFAL XENLA
20	73	7.7	166	1	ING SHEEP
21	73	7.7	326	1	VS09 ROTH
22	73	7.7	1274	1	EXF CLOBO
23	72.5	7.6	233	1	TNFA CANFA
24	72.5	7.6	233	1	TNFA MACFA
25	72.5	7.6	233	1	TNFA MACNU
26	72.5	7.6	233	1	TNFA PAPAN
27	72	7.6	234	1	TNFA CAVPO
28	72	7.6	356	1	GBA3 NEUCR
29	72	7.6	393	1	PRIL PYRAB
30	72	7.6	545	1	YB90 YEAST
31	71.5	7.5	219	1	SPRA IPOBA
32	71.5	7.5	233	1	TNFA HUMAN
33	71.5	7.5	349	1	HS2S DROME

34	71.5	7.5	525	1	AGSA APLCA
35	71	7.5	232	1	TNFA_PIG
36	71	7.5	354	1	GBA3_USTHO
37	71	7.5	354	1	GBA3_USTWA
38	71	7.5	680	1	PEP2_STRPN
39	70.5	7.4	352	1	GBA1_MAGGR
40	70.5	7.4	890	1	BCN5_CLOPE
41	70	7.4	233	1	TNFA_SAISC
42	70	7.4	1139	1	RBL2_HUMAN
43	69.5	7.3	233	1	ADRI_YEAST
44	69.5	7.3	233	1	TNFA_MARMO
45	69.5	7.3	235	1	TNFA_RABIT

#### ALIGNMENTS

RESULT 1					
TN18 HUMAN					
ID	TN18 HUMAN	STANDARD:	PRT:	177 AA.	
AC	Q9UNG2; O95852;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor ligand superfamily member 18 (Glucocorticoid-induced TNF-related ligand) (HGIRL) (Activation-inducible TNF-related ligand) (AITRL)				
DE	GN TNFSF18 OR AITRL OR GITRL OR TL6.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Umbilical vein;				
RX	MEDLINE=99175482; PubMed=10074428;				
RA	Gurney A.L., Marsters S.A., Huang A., Pitti R.M., Mark M., Baldwin D.F., Gray A.M., Dowd P., Brush J.J., Heldens S., Schow P., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J., Ashkenazi A.;				
RA	"Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR.";				
RL	Curr. Biol. 9:215-218(1999).				
RN	[2]				
RP	SEQUENCE OF 9-177 FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=99155876; PubMed=10037686;				
RA	Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., Xing L., Liu D., Wang S.-X., Kwon B.S.;				
RA	"Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand.";				
RL	J. Biol. Chem. 274:6056-6061(1999).				
CC	FUNCTION: Cytokine that binds to TNFSF18/AITR/GITR. Important for interactions between activated T lymphocytes and endothelial cells and may modulate T lymphocyte survival in peripheral tissues.				
CC	SUBUNIT: Homotrimer (Potential).				
CC	SUBCELLULAR LOCATION: Type II membrane protein (Potential).				
CC	TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE SMALL INTESTINE, OVARY, TESTIS, KIDNEY AND ENDOTHELIAL CELLS.				
CC	INDUCTION: UPREGULATED AFTER STIMULATION BY LIPOPOLYSACCHARIDES.				
CC	SIMILARITY: Belongs to the tumor necrosis factor family.				
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DR	EMBL; AF125303; AAD22634.1; -				
DR	EMBL; AF117713; AAD19625.1; -				
DR	Genew; HGNC:11932; TNFSF18.				

Feb. 25



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DR MM; 603898; --
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR008983; TNF_like.
DR PROSITE; PS00251; TNF_1; FALSE NEG.
DR PROSITE; PS00049; TNF_2; FALSE NEG.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 28 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 29 49 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 50 177 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 177 AA; 20307 MW; 3D78CEB90F4C9E3 CRC64;

Query Match 100.0%; Score 951; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 9.4e-82;
Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLSHLENPLSHSRTOGAQRSSWKLMFCSIVMLFLCSFSLIFLQLETAKPCVA 60
Db 1 MCLSHLENPLSHSRTOGAQRSSWKLMFCSIVMLFLCSFSLIFLQLETAKPCVA 60
QY 61 KFGPLPSKQWASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPPEVRLYN 120
Db 61 KFGPLPSKQWASSEPPCVNKVSDWKLEILQNGLYLYIGQVAPNANVNDVAPPEVRLYN 120
QY 121 KDMITQTLTKNSKIQNVGGTYELHVGDTIDLFNSEHQVLKNTYWGIIILANPQFIS 177
Db 121 KDMITQTLTKNSKIQNVGGTYELHVGDTIDLFNSEHQVLKNTYWGIIILANPQFIS 177

RESULT 2
TNF5_CHECK STANDARD; PRT; 272 AA.
ID TNF5_CHECK STANDARD; PRT; 272 AA.
AC Q9T8D8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
DE L) (CD154 protein).
GN TNF5 OR CD40LG OR CD40L.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Spleen;
RA Tregaskes C.A., Young J.R., Burnside J.;
RT "Cloning of a putative chicken CD40 ligand.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
CC proliferation in the absence of co-stimulus as well as IGE
CC production in the presence of IL-4. Involved in immunoglobulin
CC class switching (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PMW: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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or send an email to license@isb-sib.ch).
CC EMBL; AJ243435; CAB95748.2; --
DR HSRP; P29965; IALY.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005174; F:CD40 receptor binding; ISS.
DR GO; GO:0042100; P:B-cell proliferation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0007159; P:leukocyte cell adhesion; ISS.
DR GO; GO:0030168; P:platelet activation; ISS.
DR InterPro; IPR003263; TNF_5.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR008983; TNF_like.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01702; CD40LIGAND.
DR PRODOM; PD008600; TNF_5; 1.
DR PRODOM; PD003012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 272 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 5, MEMBRANE FORM.
FT CHAIN 111 272 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 24 44 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 45 272 EXTRACELLULAR (POTENTIAL).
FT SITE 110 111 CLEAVAGE (BY SIMILARITY).
FT DISULFID 190 229 POTENTIAL.
FT CARBOHYD 124 124 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 272 AA; 30832 MW; 8CD0338A924E044B CRC64;

Query Match 11.4%; Score 108.5; DB 1; Length 272;
Best Local Similarity 29.8%; Pred. No. 0.0063;
Matches 36; Conservative 22; Mismatches 44; Indels 19; Gaps 5;

QY 68 KQWASSEPPCVNKVS--DWKLEILQNGLYLYIGQVAPNANVNDVAPPEVRLY 118
Db 153 KW-WTTSVAPTSSLSIYHEGKLVKEAGLYIYQVSVFCTKAAASAPFTLYLYLPNEE 211
QY 119 -----KXKDMITQTLTKNSKIQNV--GGTYELHVGDT--IDLFNSEHQVLKNTYWGIIIL 169
Db 212 DRLMKGLDTHSTSTALCQLSIREGGVFLRQGMVFVNVTDTSTAVNVEGNTYFGMFK 271
QY 170 L 170
Db 272 L 272

RESULT 3
MCL1_HUMAN STANDARD; PRT; 377 AA.
ID MCL1_HUMAN STANDARD; PRT; 377 AA.
AC Q15049; Q96RPS; Q9UGY8;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Membrane protein MLC1.
GN MLC1 OR WK1 OR KIAA0027.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;

```

"Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1.";  
 DNA Res. 1:27-35(1994).  
 [2]  
 RP REVISIONS.  
 RA Ohara C., Nagase T., Kikuno R., Nomura N.,  
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.  
 RN  
 RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANT PC MET-309.  
 RC  
 RX TISSUE=Hippocampus;  
 RX MEDLINE=21225990; PubMed=11326298;  
 RA Meyer J., Huber A., Ortega G., Syagailo Y.V., Jatzke S., Schmitt A.,  
 RA Moesner R., Strom T.M., Ulzheimer-Teuber I., Stoeber G., Schmitt A.,  
 RA Lesch K.P.,  
 RA "A missense mutation in a novel gene encoding a putative cation  
 RT channel is associated with catatonic schizophrenia in a large  
 RT pedigree";  
 RL Mol. Psych. 6:302-306(2001).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX DUNHAM I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
 RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
 RA Bagguely C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
 RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,  
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor P.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
 RA Dhani P.D., Dockree C., Doldworth S.J., Durbin R.M., Ellington A.G.,  
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.P., Leversha M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
 RA McClay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
 RA Scott C.B., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,  
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen P., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,  
 RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Lareille P., Layman D., Ozereky P., Rohlfing T.,  
 RA Schuet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,  
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
 RA Peyrard M., Kedra D., Seroussi E., Franconi I., Tapia I., Bruder C.E.,  
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
 RA Khan A.S., Lane L., Tliahun Y., Wright H.,  
 RT "The DNA sequence of human chromosome 22";  
 RL Nature 402:489-495(1999).  
 RN  
 RP VARIANTS MLC LEU-93; ARG-118; ARG-212 AND LEU-280.  
 RX MEDLINE=21152271; PubMed=11254442;  
 RA Leeswater P.A.J., Yuan B.O., van der Steen J., Mulders J.,  
 RA Koenst A.A.M., Ilja Boor P.K., Meijaski-Bosnjak V.,  
 RA van der Maarel S.M., Frants R.R., Oudejans C.B.M., Schutgens R.B.H.,  
 RA Pronk J.C., van der Knapp M.S.;

"Mutations of MLC1 (KIAA0027), encoding a putative membrane protein, cause megalencephalic leukoencephalopathy with subcortical cysts.";  
 Am. J. Hum. Genet. 68:831-838(2001).  
 CC -1- FUNCTION: May be a transporter. May act as a non-selective neuronal cation channel.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: Expressed in the brain, with highest levels found in the amygdala, nucleus caudatus, thalamus and hippocampus.  
 CC -1- DISEASE: Defects in MLC1 are a cause of megalencephalic leukoencephalopathy with subcortical cysts (MLC). MLC is an autosomal recessive disorder characterized by macrocephaly, deterioration of motor functions with ataxia, and spasticity, magnifying in mental decline. The brain appears swollen on magnetic resonance imaging, with diffuse white-matter abnormalities and the invariable presence of subcortical cysts.  
 CC -1- DISEASE: Defects in MLC1 are a cause of periodic catatonias (PC), a familial subtype of catatonic schizophrenia which is a genetically heterogeneous disorder characterized by psychosis and psychomotor disturbances.  
 CC  
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 CC  
 DR EMBL; D25217; BAA04947.2; ALT INIT.  
 DR EMBL; AF319633; AAX60119.1; -  
 DR EMBL; AL022327; CAB51559.1; ALT\_INIT.  
 DR Genbank; HGNC:17082; MLC1.  
 DR MIN; 605908; -  
 DR MIN; 604004; -  
 DR GO; GO:0000299; C: integral to membrane of membrane fraction; TAS.  
 KW Transport; Transmembrane; Ionic channel; Disease mutation.  
 FT TRANSMEM 56 72  
 FT TRANSMEM 113 128  
 FT TRANSMEM 146 162  
 FT TRANSMEM 200 216  
 FT TRANSMEM 228 244  
 FT TRANSMEM 302 318  
 FT DOMAIN 262 280  
 FT DOMAIN 147 156  
 FT DOMAIN 173 176  
 FT DOMAIN 305 315  
 FT VARIANT 93 93  
 FT VARIANT 118 118  
 FT VARIANT 212 212  
 FT VARIANT 280 280  
 FT VARIANT 309 309  
 FT SEQUENCE 377 AA; 41141 MW; 9AF70B87D979F459 CRC64;  
 Query Match 9.0%; Score 85.5; DB 1; Length 377;  
 Best Local Similarity 20.8%; Pred. No. 1.3;  
 Matches 32; Conservative 31; Mismatches 54; Indels 37; Gaps 6;  
 QY 26 LWFCSIVN--LLFLCSFWLIFLQLETAKEPCMAKFGPLPSKQWASSEPPCVNKVS 83  
 Db 127 IFWGCKVLNPSAININENLILLLELLMAATVIA-----ARSEEDCKKK-- 174  
 QY 84 DWKEILONGLYLYQVAPNVDVAPFVRLYKNDKMTLTNKSQIQLNKGSTYELH 143  
 Db 175 -----KGSMSDSANILDEVPFPPARVLKSYVVEVIAGISAV--LGSIIALN 218  
 QY 144 VGDTIDLFNSHQVLKKNYWGIIILANPQFIS 177  
 Db 219 VDDSV----SGPILSV---TFPWILVACFPISA 245





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CC -----

DR EMBL; X03940; CAA25777.1; -

DR EMBL; Z46660; CAA86638.1; -

DR PIR; S49627; S49627.

DR HSSP; P12351; 1PYC.

DR GeneOnline; 142631; -

DR TRANSFAC; T00044; -

DR SGD; S0004563; ARG81.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:0003712; P:transcription cofactor activity; IDA.

DR GO; GO:0045955; P:negative regulation of calcium ion dependen. .; IDA.

DR InterPro; IPR001138; Fungi\_Tn.

DR Pfam; PF00172; Zn clus; 1.

DR SMART; SM00066; GAL4; 1.

DR PROSITE; PS00463; ZN2\_Cy6\_FUNGAL\_1; 1.

DR PROSITE; PS00463; ZN2\_Cy6\_FUNGAL\_2; 1.

DR Transcription regulation; Activator; DNA-binding; Nuclear protein.

KW Zinc; Metal-binding; Arginine metabolism.

FT DNA BIND 21 48 ZN(2)-CYS(6), FUNGAL-TYPE.

FT CONFLICT 4 4 S -> F (IN REF. 1).

FT CONFLICT 129 129 MISSING (IN REF. 1).

FT CONFLICT 283 283 F -> V (IN REF. 1).

FT CONFLICT 345 345 D -> V (IN REF. 1).

FT CONFLICT 366 366 E -> Q (IN REF. 1).

FT CONFLICT 549 549 T -> S (IN REF. 1).

FT CONFLICT 597 597 T -> S (IN REF. 1).

FT CONFLICT 665 665 K -> N (IN REF. 1).

FT CONFLICT 869 869 V -> I (IN REF. 1).

SQ SEQUENCE 880 AA; 100281 MW; DA033AB2B373FA15 CRC64;

Query Match 8.1%; Score 77.5; DB 1; Length 880;

Best Local Similarity 22.7%; Pred. NO. 19;

Matches 37; Conservative 35; Mismatches 54; Indels 37; Gaps 8;

QY 45 IFIFLQL---ETAKEPCMAK-----FGLPLSKMQMAGSEPPCVNKV----- 82

DB 555 IFSFLKLQDSLTALDKVAKELVLPSEDDNYKELDTSNATSSSPRDVVQEGLFRE 614

QY 83 ----SDWK--LEILONGLYLYGVQVAPNAN----YNDVAPPEVLYKKNKMIQTLTKSK 132

DB 615 ALNENDGKIHTEFVKETITVNSADSTPSSTPTPIFTNIA---TESYINKSDISKLVSKTD 671

QY 133 IQNVGVTYELH-VGDTIDLIHFSEHOVLKNNYTGIIILLANPQ 174

DB 672 -ENIGTDSLGLPNSLILLRSDCVIRVHNEYNTLVLPVR 713

RESULT 8

ID NBEA DROME STANDARD; PRT: 3584 AA.

AC Q9W4E2; O16024; Q81R9; Q961G8; Q9GP69; Q9GP70;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DE Neurobeachin protein (Rugose protein) (A-kinase anchor protein 550)

DE (AKAP 550) (AKAP550).

GN RG OR AKAP550 OR CG6775.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxId=7227;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS B AND S), FUNCTION, SUBUNIT, AND

RP SUBCELLULAR LOCATION.

RC TISSUE=Head.

RX MEDLINE=20855611; PubMed=11102458;

RA Wang X., Herberg F.W., Laue M.M., Wullner C., Hu B.,

RA Petrasch-Parwez B., Kiliann M.W.;

RT "Neurobeachin: a protein kinase A-anchoring, beige/Chediak-Higashi

RT protein homolog implicated in neuronal membrane traffic.";

RL J. Neurosci. 20:8551-8565(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Berkely;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,

RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glöckle A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [3]

RP REVISIONS, AND ALTERNATIVE SPLICING.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review.";

RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).

RN [4]

RP SEQUENCE OF 1-2389 FROM N.A. (ISOFORMS B AND S), FUNCTION, SUBUNIT,

RP SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.

RC STRAIN=Canlon-S; TISSUE=Embryo;

RX MEDLINE=97476266; PubMed=9334242;

RA Han J.-D., Baker N.E., Rubin C.S.;

RT "Molecular characterization of a novel A kinase anchor protein from

RT Drosophila melanogaster.";

RL J. Biol. Chem. 272:26611-26619(1997).

RN [5]



RA D'Yall-Smith M.L., Holmes I.H.:  
RT "Sequence homology between human and animal rotavirus  
RT serotype-specific glycoproteins.";  
RN Nucleic Acids Res. 12:3973-3982(1984).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
RA Chanock R.M., Flores J.;  
RT "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -!- FUNCTION: VP7 is the major neutralization antigen.  
CC -!- SUBCELLULAR LOCATION: Rough endoplasmic reticulum.  
CC -!- SIMILARITY: Belongs to the rotaviruses VP7 protein family.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL; X00572; CRA25236.1; -;  
DR EMBL; A01028; CRA00124.1; -;  
DR PIR; G27620; VGRXHU.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
DR Coats protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37202 MW; 2D43B6BEC86FCB0 CRC64;  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 6.7;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
QY 26 LWFCSIVMLFLC-----SPSWLIFIFLOLETAKEPCMAK-----FGPLPSKQWQ 71  
DB 10 LTILISILNLYLKTIITNTWDYIIFRLLIALISPFVTRQNYGMVLPITGSLDAYTN 69  
QY 72 ASSEPP-----CV-----NKVSDWKLEILQGLYLYGVAPNA---NYNDVAPFEV 115  
DB 70 STSGEPFLTSLCLYPAEAKNEISDDEWNTLSQLETKGPIGVSVYFYDNDINTFSV 129  
QY 116 --RLYKNKDMIQTLNKSQIENVGTYELHVGDTIDLFNSEHQVLKNTYWGILLANP 173  
DB 130 NPQLYCDNVV-----LMRYDNTSELDAELADILNE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171  
RESULT 10  
ID VS09\_ROTHD STANDARD; PRT; 326 AA.  
AC P11950;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Glycoprotein VP7 (Serotype-specific antigen) (Outer shell  
DE glycoprotein).  
GN S9.  
OS Human rotavirus (serotype 2 / strain DS1).  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10950;  
RN [1]  
RP SEQUENCE FROM N.A.  
QY 26 LWFCSIVMLFLC-----SPSWLIFIFLOLETAKEPCMAK-----FGPLPSKQWQ 71  
DB 10 LTILISILNLYLKTIITNTWDYIIFRLLIALISPFVTRQNYGMVLPITGSLDAYTN 69  
QY 72 ASSEPP-----CV-----NKVSDWKLEILQGLYLYGVAPNA---NYNDVAPFEV 115  
DB 70 STSGEPFLTSLCLYPAEAKNEISDDEWNTLSQLETKGPIGVSVYFYDNDINTFSV 129  
QY 116 --RLYKNKDMIQTLNKSQIENVGTYELHVGDTIDLFNSEHQVLKNTYWGILLANP 173  
DB 130 NPQLYCDNVV-----LMRYDNTSELDAELADILNE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171  
RESULT 11  
ID VS09\_ROTHD STANDARD; PRT; 326 AA.  
AC P11851;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Glycoprotein VP7 (Serotype-specific antigen) (Outer shell  
DE glycoprotein).  
GN S9.  
OS Human rotavirus (serotype 2 / strain HN126).  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10951;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
RA Chanock R.M., Flores J.;  
RT "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -!- FUNCTION: VP7 is the major neutralization antigen.  
CC -!- SUBCELLULAR LOCATION: Rough endoplasmic reticulum.  
CC -!- SIMILARITY: Belongs to the rotaviruses VP7 protein family.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
DR Coats protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 6.7;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
RA Chanock R.M., Flores J.;  
RT "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -!- FUNCTION: VP7 is the major neutralization antigen.  
CC -!- SUBCELLULAR LOCATION: Rough endoplasmic reticulum.  
CC -!- SIMILARITY: Belongs to the rotaviruses VP7 protein family.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
DR Coats protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 6.7;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;  
QY 26 LWFCSIVMLFLC-----SPSWLIFIFLOLETAKEPCMAK-----FGPLPSKQWQ 71  
DB 10 LTILISILNLYLKTIITNTWDYIIFRLLIALISPFVTRQNYGMVLPITGSLDAYTN 69  
QY 72 ASSEPP-----CV-----NKVSDWKLEILQGLYLYGVAPNA---NYNDVAPFEV 115  
DB 70 STSGEPFLTSLCLYPAEAKNEISDDEWNTLSQLETKGPIGVSVYFYDNDINTFSV 129  
QY 116 --RLYKNKDMIQTLNKSQIENVGTYELHVGDTIDLFNSEHQVLKNTYWGILLANP 173  
DB 130 NPQLYCDNVV-----LMRYDNTSELDAELADILNE-----W-----LCNP 167  
QY 174 QFIS 177  
DB 168 MDIS 171  
RESULT 11  
ID VS09\_ROTHD STANDARD; PRT; 326 AA.  
AC P11851;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Glycoprotein VP7 (Serotype-specific antigen) (Outer shell  
DE glycoprotein).  
GN S9.  
OS Human rotavirus (serotype 2 / strain HN126).  
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.  
OX NCBI\_TaxID=10951;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88044489; PubMed=2823458;  
RA Green K.Y., Midthun K., Gorziglia M., Hoshino Y., Kapikian A.Z.,  
RA Chanock R.M., Flores J.;  
RT "Comparison of the amino acid sequences of the major neutralization  
RT protein of four human rotavirus serotypes.";  
RL Virology 161:153-159(1987).  
CC -!- FUNCTION: VP7 is the major neutralization antigen.  
CC -!- SUBCELLULAR LOCATION: Rough endoplasmic reticulum.  
CC -!- SIMILARITY: Belongs to the rotaviruses VP7 protein family.  
DR InterPro; IPR001963; VP7.  
DR Pfam; PF00434; VP7; 1.  
DR ProDom; PD000191; VP7; 1.  
DR Coats protein; Transmembrane; Glycoprotein.  
KW TRANSMEM 32 48  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 326 AA; 37216 MW; 5D338B3BE9D6A9B5 CRC64;  
Query Match 8.1%; Score 77; DB 1; Length 326;  
Best Local Similarity 22.8%; Pred. No. 6.7;  
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;



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FT CARBOHYD 238 238 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 326 AA; 37246 MW; 4799219EE9D6A9B1 CRC64;

Query Match
Best Local Similarity 22.8%; Score 77; DB 1; Length 326;
Matches 42; Conservative 29; Mismatches 59; Indels 54; Gaps 9;

QY 26 LMLFCSIVMLFLC-----SFSWLIIFIQLETAKEPCVAK-----FGLPSKWMQ 71
Db 10 LTLISLILNLYLTKITNTMDIIFRLLLIALLISFVVRTQNYGYLPITGSLDAVYN 69

QY 72 ASSEPP-----CV-----NKVSDWKLEILONGLYIGQVAPNA---NYNDVAPPEV 115
Db 70 STSGEPLTCLLYPTEAKNISDEWENTLSQLFKGWPIGSVYFKYNDINTFSV 129

QY 116 --RLYKNQMIQLTNKSQKQNGVGYVELHVGDTIDLIENSEHQLVKNNTYGIILLANP 173
Db 130 NPQLYCDYVNV-----LMRYDNTSETDASELADLILNE-----W-----LCNP 167

QY 174 QFIS 177
Db 168 MDIS 171

RESULT 12
TNFA_PAPHU STANDARD; PRT; 233 AA.
AC 07510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 18-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSP2 OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciae;
OC Cercopitheciae; Papio.
OX NCBI_TaxID=36229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147379; PubMed=9488055;
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT alpha."
RL Mol. Immunol. 34:1041-1042(1997).

CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC EMBL; AF019963; AAC31675.1; -.
CC HSSP; P01375; 4TSV.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR008636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 233
FT DOMAIN 7 233
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT FT
FT DOMAIN 57 233
FT SITE 76 77
FT MOD_RES 2 2
FT DISULFID 145 177
FT SQ SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match
Best Local Similarity 21.8%; Score 76.5; DB 1; Length 233;
Matches 50; Conservative 34; Mismatches 70; Indels 75; Gaps 11;

QY 7 ENMLSHSRITQAGRSWKMLFCSIVMLFLCFSFSLIFFL---QLETAKEPCMAKFG 63
Db 15 EALPKRTAGPQGSRR-CWFLSLFSLIVAGATTFLCLHFGVIGPQREPPKDFSL--IS 71

QY 64 PLPSKQWAS---SEPPCVN-----KVSDMKLETLQNL 94
Db 72 PLAQVRSRSTPDSKPVHVVPANPQAGQLNRRANALLANGVELDQLVVPSEGL 131

QY 95 YLYIQGV-----APNANY---NDVAPFEVLYKXKMDIOTLTNKSQKN----- 135
Db 132 YLYIQGVLFKGGCGPSNHVLLTHITRIASVYQTKVLLSAI--KSPQRETPEGAEAKP 189

QY 136 -----VGGTYELHVGDTID-----LIENSEHQLVKNNTYGIILL 170
Db 190 WYEPIYLGQVFLKGGKGLSALINLPDYLDFAESGQV-----YFGITAL 233

RESULT 13
V061_F0W6V STANDARD; PRT; 129 AA.
ID V061_F0W6V
AC P21972;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative CC-type chemokine FPV061.
GN FPV061 OR FPI4
OS Fowlpox virus (FPV).
OS Viruses; GEDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FP-1;
RX MEDLINE=90324937; PubMed=2165135;
RA Tartaglia J., Winslow J., Goebel S., Johnson G.P., Taylor J.,
RA Paoletti E.;
RT "Nucleotide sequence analysis of a 10.5 kbp HindIII fragment of
RT fowlpox virus: relatedness to the central portion of the vaccinia
RT virus HindIII D region."
RL J. Gen. Virol. 71:1517-1524(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;

```



RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;  
 RT "The genome of fowlpox virus."  
 RL J. Virol. 74:3815-3831(2000).  
 CC -!- SIMILARITY: LOW SIMILARITY TO THE INTERCRINE BETA FAMILY (SMALL  
 CC CYTOKINE C-C) (CHEMOKINE CC).  
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 CC -----  
 CC EMBL; X17202; CAA3065.1; --  
 DR EMBL; AF198100; AAP44405.1; --  
 DR PIR; B35216; B35216.  
 DR InterPro; IPR001811; Chemokine\_IL8.  
 KW Hypothetical protein; Cytokine.  
 CC SEQUENCE 129 AA; 14110 MW; E0C2E5E79875B40DB CRC64;  
 CC -----  
 CC Query Match 7.9%; Score 75; DB 1; Length 129;  
 CC Best Local Similarity 28.8%; Pred. No. 3.6;  
 CC Matches 23; Conservative 14; Mismatches 37; Indels 6; Gaps 3;  
 CC -----  
 CC 31 SIYVLLFLCSFSLIFLQLETAKEPCMAKFGPLPSKQW--ASSEPCCVKNKVSQDWKL 87  
 CC 6 SIYVLTIGSCFYNPFI-LTYECRDCDCNGRYGVPAPKVLNCTKTPGCPD--SGYLL 62  
 CC 88 BILQNGLYLYGQVAPNANY 107  
 CC 63 TTSENKTYCITGNETDKGY 82  
 CC -----  
 CC RESULT 14  
 CC TNFA\_PAPSP STANDARD; PRT; 233 AA.  
 ID P33620;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor  
 DE ligand superfamily member 2) (TNF-a) (Cachectin).  
 GN TNF OR TNFSF2 OR TNFA.  
 OS Papio sp. (Baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=61183;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sanjanwala M., Edwards A.;  
 RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and  
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can  
 CC induce cell death of certain tumor cell lines. It is potent  
 CC pyrogen causing fever by direct action or by stimulation of  
 CC interleukin 1 secretion and is implicated in the induction of  
 CC cachexia. Under certain conditions it can stimulate cell  
 CC proliferation and induce cell differentiation.  
 CC -!- SUBUNIT: Homotrimer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an  
 CC extracellular soluble form (By similarity).  
 CC -!- PTM: The soluble form derives from the membrane form by  
 CC proteolytic processing (By similarity).  
 CC -!- PTM: The membrane form, but not the soluble form, is  
 CC phosphorylated on serine residues. Dephosphorylation of the  
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By  
 CC similarity).  
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.  
 CC -----  
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 CC -----  
 CC EMBL; X62141; CAA44068.1; --  
 DR PIR; S22052; S22052.  
 DR HSP; P01375; IABM.  
 DR InterPro; IPR006053; TNF\_abc.  
 DR InterPro; IPR006052; TNF\_family.  
 DR InterPro; IPR008983; TNF\_like.  
 DR InterPro; IPR003636; TNF\_subf.  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNFCROSISCT.  
 DR PRODOM; PD002012; TNF\_subf; 1.  
 DR SMART; SM00207; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS00049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.  
 FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.  
 FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.  
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).  
 FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).  
 FT MOD\_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).  
 FT DISULFID 145 177 BY SIMILARITY.  
 CC SEQUENCE 233 AA; 25557 MW; 455360B48DC74173 CRC64;  
 CC -----  
 CC Query Match 7.8%; Score 74.5; DB 1; Length 233;  
 CC Best Local Similarity 21.2%; Pred. No. 7.8;  
 CC Matches 51; Conservative 28; Mismatches 63; Indels 99; Gaps 12;  
 CC -----  
 CC 7 ENWPLSHSRTOGAQRSSWKMLFCSIVMLFLCSFSL-----IFLQL----- 51  
 CC 15 EALPKTKGPGQSR-----CLFLSFLVAGATLFLCLHFGVIGPORE 61  
 CC 52 EAKEPCMAKFGPLPSKQMAS--SEPPCVNKVS----- 83  
 CC 62 EFPKPSL--ISPLAQAVRSRSTPSDKFVAHVANQAQGLQWLNRANALLANGVEL 119  
 CC 84 -DWKLEILQNGLYLYGQV-----APNANY---NDVAPFVRLYKNKDMQTLTKSKI 133  
 CC 120 RNQLWPSEGLYLYSVLFKQGCPSTHVLTHITISRIAVSYOTKVNLSAI--KSPC 177  
 CC 134 QN-----VGGTYELHVGDTID-----LIFNSEHVLKNTYWGIL 169  
 CC 178 QRETPGEAKPWEPVILGVGFQLEKGRLSAEINLPDYLDFAESGV-----YFGIIA 232  
 CC -----  
 CC 170 L 170  
 CC 233 L 233  
 CC -----  
 CC RESULT 15  
 CC SCSD\_TOBAC STANDARD; PRT; 271 AA.  
 ID SCSD\_TOBAC  
 AC Q9ZT29;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Delta-7-sterol-C5(6)-desaturase (EC 1.3.3.-) (Delta-7-C-5 sterol  
 DE desaturase) (Delta-7-sterol-C5-desaturase).  
 DE Nicotiana tabacum (Common tobacco).  
 OS Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 CC [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=cv. Xanthi; TISSUE=Callus;  
 RC

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RX MEDLINE=9927392; PubMed=10344195;
RT Husselstein T., Schaller H., Gachotte D., Benveniste P.;
RA Delta7-sterol-C5-desaturase: molecular characterization and
RT functional expression of wild-type and mutant alleles.";
RL Plant Mol. Biol. 39:891-906(1999).
CC -!- FUNCTION: Involved in the biosynthesis of sitosterol and
CC campesterol.
CC -!- COFACTOR: iron (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum (Probable).
CC -!- DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -!- SIMILARITY: Belongs to the sterol desaturase family.
CC -----
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CC -----
CC EMBL: AF081794; AAD04034.1; -
CC InterPro: IPR006087; Sterol_desat.
CC DR InterPro: IPR006088; Sterol_desatur.
CC Pfam: PF01598; Sterol_desat; 1.
CC Sterol biosynthesis; Oxidoreductase; Endoplasmic reticulum; Iron;
CC Transmembrane.
CC KW TRANSMEM 44 64 POTENTIAL.
CC FT TRANSMEM 120 140 POTENTIAL.
CC FT TRANSMEM 190 210 POTENTIAL.
CC FT DOMAIN 144 148 HISTIDINE BOX-1.
CC FT DOMAIN 158 162 HISTIDINE BOX-2.
CC FT DOMAIN 235 239 HISTIDINE BOX-3.
CC SQ SEQUENCE 271 AA; 31842 MW; 361520EAAB56D86F CRC64;
CC -----
Query Match 7.8%; Score 74.5; DB 1; Length 271;
Best Local Similarity 22.7%; Pred No.9,3;
Matches 34; Conservative 23; Mismatches 50; Indels 43; Gaps 9;
CC -----
QY 10 PLSHSTQGAQRSSWKWL--FCGIVLLFLCFSWLIFF----- 48
DB 31 PLFH-MLQG-----WLRNYTGGVLLYFISGLFCFYIHLKRNWYTPKDAIPSNKAM 81
QY 49 -LQLETAKEPCMAKFGPLP--SKWQVASSPEPCNVKSPD--WKLEILQNLGLYLI---YQG 100
DB 82 LQIQSVAMK-AMFYCALPSELSEYHENGWTKCFARISDVGWLSUYIYAAILVIVEFGI 140
QY 101 VAPNANYNDVAPFEVRLYKQKDMIQTLTNK 130
DB 141 YNMHMLHDIKP----LYKYLHATHIYNNK 166

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